

SEQUENCE LISTING

<110> Renner, Wolfgang A.
Bachmann, Martin
Tissot, Alain
Maurer, Patrick
Lechner, Franziska
Sebbel, Peter
Piossek, Christine

<120> Molecular Antigen Array

<130> 1700.0190004

<140> (To be assigned)
<141> 2002-01-18

<150> US 60/262,379
<151> 2001-01-19

<150> US 60/288,549
<151> 2001-05-04

<150> US 60/326,998
<151> 2001-10-05

<150> US 60/331,045
<151> 2001-11-07

<160> 350

<170> PatentIn Ver. 2.1

<210> 1
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<400> 1
ggggacgcgt gcagcaggta accaccgtta aagaaggcac c

41

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 2
cggtggttac ctgctgcacg cgttgcttaa gcgacatgta gcgg

44

<210> 3
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 3
ccatgaggcc tacgataccc 20

<210> 4
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<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 4
ggcactcacg gcgcgttta caggc 25

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<223> Description of Artificial Sequence: Primer

<400> 5
ccttcattaa cggtggttac ctgctggcaa ccaacgtgg tcatgac 47

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<223> Description of Artificial Sequence: Primer

<400> 6
aagcatgctg cacgcgtgtg cggtggtcgg atcgccccgc 40

<210> 7
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer

<400> 7
gggtcttagat tcccaaccat tcccttatcc aggcttttg acaacgctat gctccgcgcc 60
catcgctgc accagctggc ctttgacacc 90

<210> 8
<211> 108
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer

<400> 8
gggtctagaa ggaggtaaaa aacgatgaaa aagacagcta tcgcgattgc agtggcactg 60
gctggtttcg ctaccgtagc gcaggccttc ccaaccattc ccttatcc 108

<210> 9
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
cccgaaattcc tagaagccac agctgccctc c 31

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
cctgcggtgtt tctgaccgac accc 24

<210> 11
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ccgcggaaga gccaccgcaa ccaccgtgtg ccgccaggat g 41

<210> 12
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
ctatcatcta gaatgaatag aggattcttt aac 33

<210> 13
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified ribosome
binding site

<400> 13
aggaggtaaa aaacg

15

<210> 14
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: signal peptide

<400> 14
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15
Thr Val Ala Gln Ala
20

<210> 15
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: modified Fos
construct

<400> 15
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
1 5 10 15
Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
20 25 30
Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
35 40 45

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide linker

<400> 16
Ala Ala Ala Ser Gly Gly
1 5

<210> 17
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide linker

<400> 17
Gly Gly Ser Ala Ala Ala

1 5

<210> 18
<211> 256
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 18
gaattcagga ggtaaaaaac gatgaaaaag acagctatcg cgattgcagt ggcactggct 60
ggtttcgcta ccgttagcga ggcctgggtg gggccggccg cttctggtgg ttgcggtggt 120
ctgaccgaca ccctgcaggc gaaaccgac caggtggaaag acaaaaaatc cgcgctgcaa 180
accgaaatcg cgaacctgct gaaagaaaaa gaaaagctgg agttcatcct ggcggcacac 240
ggtggttgc aagctt 256

<210> 19
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 19
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
5 10 15
Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30
Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
35 40 45

His Gly Gly Cys
50

<210> 20
<211> 261
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<220>
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<222> (22)..(240)

<400> 20
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Met Lys Lys Thr Ala Ile Ala Ile Ala Val
1 5 10
gca ctg gct ggt ttc gct acc gta gcg cag gcc tgc ggt ggt ctg acc 99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Cys Gly Gly Leu Thr
15 20 25

gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc gcg	147
Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala	
30	35
	40
ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg gag	195
Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu	
45	50
	55
ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct	240
Phe Ile Leu Ala Ala His Gly Gly Cys Gly Ser Ala Ala Ala	
60	65
	70
gggtgtgggg atatcaagct t	261

<210> 21
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<400> 21
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15
Thr Val Ala Gln Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
20 25 30
Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala
35 40 45
Asn Leu Leu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His
50 55 60
Gly Gly Cys Gly Ser Ala Ala Ala
65 70

<210> 22
<211> 196
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion construct

<220>
<221> CDS
<222> (34) .. (189)

<400> 22
gaattcagga ggtaaaaaga tatcgggtgt ggg gcg gcc gct tct ggt tgc 54
Ala Ala Ala Ser Gly Gly Cys
1 5
ggt ggt ctg acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac 102
Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp
10 15 20

gaa aaa tcc gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa 150
Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys
25 30 35

gaa aag ctg gag ttc atc ctg gcg gca cac ggt ggt tgc taagctt 196
Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
40 45 50

<210> 23
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 23
Ala Ala Ala Ser Gly Gly Cys Gly Leu Thr Asp Thr Leu Gln Ala
1 5 10 15
Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30
Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
35 40 45
His Gly Gly Cys
50

<210> 24
<211> 204
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 24
gaattcagga ggtaaaaaac gatggcttgc ggtggctctga ccgacacccct gcaggcgaa 60
accgaccagg tggaagacga aaaatcccgctg cttccaaaccg aaatcgcaa cctgctgaaa 120
gaaaaaagaaa agctggagtt catcctggcg gcacacggtg gttgcgggtgg ttctgcggcc 180
gctgggtgtg gggatataa gctt 204

<210> 25
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 25
Lys Thr Met Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr
1 5 10 15
Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn

20	25	30	
Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly			
	35	40	45
Gly Cys Gly Gly Ser Ala Ala Ala			
	50	55	

<210> 26
<211> 26
<212> PRT
<213> *Homo sapiens*

<400> 26
 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
 1 5 10 15

 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
 20 25

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<210> 27
<211> 262
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 27
gaattcaggc ctatggctac aggctcccg aggctccctgc tcctggcttt tggcctgctc 60
tgcctgccct ggcttcaaga gggcagcgcgt ggggtgtgggg cggccgcgttc tggtgttgtgc 120
ggtggtctga ccgcacaccct gcaggcgaa accgaccagg tggaaagacga aaaatccgcg 180
ctgcaaaccg aaatcgcgaa cctgctgaaa gaaaaagaaaa agctggagtt catcctggcg 240
gcacacggtg gttgctaagc tt 262

<210> 28
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 28
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
5 10 15

Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
35 40 45

His Gly Gly Cys
50

<210> 29

<211> 261
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<220>
<221> CDS
<222> (7)..(240)

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<400> 29
gaattc atg gct aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc      48
    Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly
    1           5           10

ctg ctc tgc ctg ccc tgg ctt caa gag ggc agc gct tgc ggt ggt ctg      96
Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu
    15          20          25          30

acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc     144
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser
    .           35          40          45

gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg     192
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
    50          55          60

gag ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct     240
Glu Phe Ile Leu Ala Ala His Gly Gly Cys Gly Ser Ala Ala Ala
    65          70          75

gggtatggaa qqcctaagct t                                         261

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<210> 30
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

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<400> 30
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
      5          10          15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu Thr Asp
      20          25          30

Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu
      35          40          45

Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
      50          55          60

Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
      65          70          75

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<210> 31
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
cctgggtggg ggccggccgct tctgggtggtt gcgggtggtct gacc

44

<210> 32
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
ggtgggaatt caggaggtaa aaagatatcg ggtgtggggc ggcc

44

<210> 33
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
ggtgggaatt caggaggtaa aaaacgtatgg ctgcgggtgg tctgacc

47

<210> 34
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
gcttcgggtg gtctgacc

18

<210> 35
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
ccaccaagct tagcaaccac cgtgtgc

27

<210> 36
<211> 54
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 36
ccaccaagct tgatatcccc acacccagcg gccgcagaac caccgcaacc accg 54

<210> 37
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 37
ccaccaagct taggcctccc acacccagcg gc 32

<210> 38
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 38
ggtgggaatt caggaggtaa aaaacgatg 29

<210> 39
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 39
ggtgggaatt caggcctatg gctacaggct cc 32

<210> 40
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 40
ggtgggaatt catggctaca ggctccc 27

<210> 41
<211> 59
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 41
gggtctagaa tggctacagg ctcccgacg tccctgctcc tggctttgg cctgctctg 59

<210> 42
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
cgcaggcctc ggcactgccc tcttgaagcc agggcaggca gagcaggcca aaagccag 58

<210> 43
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified bee
venom phospholipase A2

<220>
<221> CDS
<222> (1)...(402)

<400> 43
atc atc tac cca ggt act ctg tgg tgt ggt cac ggc aac aaa tct tct 48
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15

ggc ccg aac gaa ctc ggc cgc ttt aaa cac acc gac gca tgc tgt cgc 96
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30

acc cag gac atg tgt ccg gac gtc atg tct gct ggt gaa tct aaa cac 144
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45

ggg tta act aac acc gct tct cac acg cgt ctc agc tgc gac tgc gac 192
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60

gac aaa ttc tac gac tgc ctt aag aac tcc gcc gat acc atc tct tct 240
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65 70 75 80

tac ttc gtt ggt aaa atg tat ttc aac ctg atc gat acc aaa tgt tac 288
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95

aaa ctg gaa cac ccg gta acc ggc tgc ggc gaa cgt acc gaa ggt cgc 336
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110

tgc ctg cac tac acc gtt gac aaa tct aaa ccg aaa gtt tac cag tgg 384
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

ttc gac ctg cgc aaa tac 402
Phe Asp Leu Arg Lys Tyr
130

<210> 44
<211> 134
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified bee
venom phospholipase A2

<400> 44
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65 70 75 80
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125
Phe Asp Leu Arg Lys Tyr
130

<210> 45
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 45 19
ccatcatcta cccaggtac

<210> 46
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 46
cccacaccca gcggccgcgt atttgcgcag gtcg 34

<210> 47
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
cggtggttct gcggccgcta tcatctaccc aggtac 36

<210> 48
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
ttagtatttg cgcaaggatcg 19

<210> 49
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 49
ccggctccat cggcgcag 18

<210> 50
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 50
accaccagaa gcggccgcag gggaaacaca tctgcc 36

<210> 51
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 51

cgggttgtct	cgccgcgtg	gctccatcg	tgca	35
<210> 52				
<211> 21				
<212> DNA				
<213> Artificial Sequence				
<220>				
<223> Description of Artificial Sequence: Primer				
<400> 52				21
ttaaggggaa acacatctgc c				
<210> 53				
<211> 33				
<212> DNA				
<213> Artificial Sequence				
<220>				
<223> Description of Artificial Sequence: Primer				
<400> 53				33
actagtctag aatgagagtg aaggagaaaat atc				
<210> 54				
<211> 42				
<212> DNA				
<213> Artificial Sequence				
<220>				
<223> Description of Artificial Sequence: Primer				
<400> 54				42
tagcatgcta gcaccgaatt tatctaattc caataattct tg				
<210> 55				
<211> 51				
<212> DNA				
<213> Artificial Sequence				
<220>				
<223> Description of Artificial Sequence: Primer				
<400> 55				51
gtagcaccca ccaaggcaaa gctgaaagct acccagctcg agaaaactggc a				
<210> 56				
<211> 48				
<212> DNA				
<213> Artificial Sequence				
<220>				
<223> Description of Artificial Sequence: Primer				
<400> 56				48
caaagctcct attcccactg ccagttctc gagctggta gctttcag				

<210> 57
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 57
ttcggtgcta gcgggtggctg cggtggtctg accgac

36

<210> 58
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 58
gatgcgtgggc ccttaaccgc aaccaccgtg tgccgcc

37

<210> 59
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: JUN amino acid sequence

<400> 59
Cys Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
1 5 10 15

Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
20 25 30

Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Gly Cys
35 40 45

<210> 60
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FOS amino acid sequence

<400> 60
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
1 5 10 15

Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
20 25 30

Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
35 40 45

<210> 61
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 61
ccggaattca tgtgcgggtgg tcggatcgcc cg 33

<210> 62
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 62
gtcgctaccc gcggctccgc aaccaacgtg gttcatgac 39

<210> 63
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 63
gttggttgcg gagccgcggg tagcgacatt gaccctata aagaatttgg 50

<210> 64
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 64
cgcgtcccaa gcttctacgg aagcggtgat aggatagg 38

<210> 65
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 65
ctagccgcgg gttgcgggtgg tcggatcgcc cg 33

<210> 66
<211> 38
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 66
cgcgtcccaa gcttttagca accaacgtgg ttcatgac 38

<210> 67
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 67
ccggaattca tggacattga cccttataaa g 31

<210> 68
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 68
ccgaccaccc caacccgcgg ctagcgaaag cgttgatagg atagg 45

<210> 69
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 69
ctaattggatc cgggtggggc tgcggtggtc ggatcgcccg gctcgag 47

<210> 70
<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 70
gtcgctaccc gcggctccgc aaccaacgtg gttcatgac 39

<210> 71
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 71
ccggaattca tggacattga cccttataaa g 31

<210> 72
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 72
ccgaccaccc cagccccac cgatccatt agtacccacc caggtacg 48

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 73
tttgttgcg gagccgcgg tagcgaccta gtatcagtt atgtc 45

<210> 74
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 74
cgcgcccaa gtttctacgg aagcggtgat aggatagg 38

<210> 75
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 75
ctagccgcgg gttgcgggtgg tcggatcgcc cg 33

<210> 76
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 76

cgcgtcccaa gcttttagca accaacgtgg ttcatgac	38
<210> 77	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 77	
ccggattca tggccacact tttaaggagc	30
<210> 78	
<211> 38	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 78	
cgcgtcccaa gcttttagca accaacgtgg ttcatgac	38
<210> 79	
<211> 31	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 79	
ccggattca tggacattga cccttataaa g	31
<210> 80	
<211> 51	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 80	
cctagagcca ccttgccac catcttctaa attagtaccc acccaggtag c	51
<210> 81	
<211> 48	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Primer	
<400> 81	
gaagatggtg gcaaagggtgg ctctagggac ctagtagtca gttatgtc	48

<210> 82
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 82
cgcgtcccaa gcttctaaac aacagtagtc tccggaag 38

<210> 83
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 83
gccgaattcc tagcagctag caccgaattt atctaa 36

<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 84
ggttaagtgc acatgagagt gaaggagaaa tat 33

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 85
taaccgaatt caggaggtaa aaagatatgg 30

<210> 86
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 86
gaagtaaagc tttaaccac cgcaaccacc agaag 35

<210> 87
<211> 33
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 87

tcgaatgggc cctcatcttc gtgtgctagt cag

33

<210> 88

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fos fusion construct

<400> 88

Glu Phe Arg Arg
1

<210> 89

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 89

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Gly Ser Gln Cys

180

<210> 90
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 90
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
65 70 75 80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Pro Ala Tyr Arg Pro Thr Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu Thr Cys Val Ile Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160
Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175
Gln Ser Arg Gly Ser Gln Cys
180

<210> 91
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 91
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 92
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 92
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 93
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 93
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Thr Asp Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110
Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160
Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175
Gln Ser Arg Glu Ser Gln Cys
180

<210> 94
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 94

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 95

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 95

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 96
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 96
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro Gln
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 97

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 97

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Lys Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Gly Ser Gln Cys
210

<210> 98
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 98
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Asp Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Ser Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 99
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 99
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 100

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 100

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg His Ala Ile Leu Cys Trp Gly Asp Leu Arg Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 101
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 101
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Gln Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Cys
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 102
<211> 183
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
human Hepatitis B construct

<400> 102

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 103

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 103

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

COMING SOON

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Ser
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 104

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 104

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 105

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 105

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 106

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 106

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys

35

40

45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 107

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 107

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 108
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 108
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 109
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 109
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Thr Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ala Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 110
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 110
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Phe Glu Cys Ser Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 111
<211> 212
<212> PRT
<213> Hepatitis B virus

<220>
<221> UNSURE
<222> (28)
<223> May be any amino acid.

<400> 111
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Xaa Asp Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Ile Thr
85 90 95

Leu Ser Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Thr Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 112

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 112

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 113

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 113

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Cys Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 114

<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 114
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Pro Gln Cys
210

<210> 115
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 115
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Ser Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 116
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 116
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

<210> 117
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 117

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Lys Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 118
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 118
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
50 55 60
Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 119
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 119
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Met Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Tyr Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Thr Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Gln Asp Pro Thr
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Val Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Val Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Gln Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 120

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 120

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg His Val Phe Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 121

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 121

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Thr Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 122

<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 122
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Ile Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 123
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 123
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Val
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Ala Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 124
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 124
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Asn
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110

Leu Val Val Gly Tyr Val Asn Thr Thr Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 125
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 125
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 126
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 126
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr

1

5

10

15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Ala Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Ile Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 127

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 127

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Thr Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 128
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 128
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Arg Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Thr Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 129
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 129
Met Gln Leu Phe His Leu Cys Leu Val Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 130

<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 130
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Ala Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 131
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 131
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ala Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 132
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 132
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Gly Ser Gln Cys
180

<210> 133
<211> 3221
<212> DNA
<213> Hepatitis B virus

<220>
<221> CDS
<222> (1901)..(2458)

<400> 133
ttccactgcc ttccaccaag ctctgcagga ccccagagtc aggggtctgt atttcctgc 60
tggtggtcc agttcaggaa cagtaaaccc tgctccgaat attgcctctc acatctcg 120
aatctccg 180
aggacctg 240
aggacctg 300
tggccaaaat 360
tcgcagtccc 420
atgcctcatc 480
aattccagga 540
aggcaactct 600
tattccatc 660
tttcttttgg 720
tggttggctt 780
gagtccttt 840
aaca 900
ggaacattgc 960
gttaacaggc 1020
gctccattta 1080
aaacaggctt 1140
ctttaccccg 1200
actgggtggg 1260
ccgatccata 1320
ctcatcgaa 1380

ttccaccaag ctctgcagga ccccagagtc aggggtctgt atttcctgc
tggtggtcc agttcaggaa cagtaaaccc tgctccgaat attgcctctc acatctcg
aatctccg 180
aggacctg 240
aggacctg 300
tggccaaaat 360
tcgcagtccc 420
atgcctcatc 480
aattccagga 540
aggcaactct 600
tattccatc 660
tttcttttgg 720
tggttggctt 780
gagtccttt 840
aaca 900
ggaacattgc 960
gttaacaggc 1020
gctccattta 1080
aaacaggctt 1140
ctttaccccg 1200
actgggtggg 1260
ccgatccata 1320
ctcatcgaa 1380

ctaggctgta ctgccaactg gatccttcgc gggacgtcct ttgtttacgt cccgtcggcg 1440
ctgaatcccg cggacgaccc ctctcggggc cgcttggac tctatcgcc ccttctccgt 1500
ctgccgttcc agccgaccac ggggcgcacc tctcttacg cggctcccc gtctgtgcct 1560
tctcatctgc cggccgtgt gcacttcgct tcacctctgc acgttgcatt gagaccaccg 1620
tgaacgccc tcagatcctg cccaaggct tacataagag gactcttggaa ctccccagcaa 1680
tgtcaacgac cgacccgtgag gcctacttca aagactgtgt gtttaaggac tgggaggagc 1740
tggggagga gattaggta aaggtcttg tattaggagg ctgttaggcat aaattggct 1800
gcgcaccagg accatgcaac ttttcacct ctgcctaattt atctcttgc catgtccac 1860
tgttcaagcc tccaaagctgt gccttgggtg gctttgggc atg gac att gac cct 1915
Met Asp Ile Asp Pro
1 5

tat aaa gaa ttt gga gct act gtg gag tta ctc tcg ttt ttg cct tct 1963
Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser
10 15 20

gac ttc ttt cct tcc gtc aga gat ctc cta gac acc gcc tca gct ctg 2011
Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu
25 30 35

tat cga gaa gcc tta gag tct cct gag cat tgc tca cct cac cat act 2059
Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr
40 45 50

gca ctc agg caa gcc att ctc tgc tgg ggg gaa ttg atg act cta gct 2107
Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala
55 60 65

acc tgg gtg ggt aat aat ttg gaa gat cca gca tcc agg gat cta gta 2155
Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val
70 75 80 85

gtc aat tat gtt aat act aac atg ggt tta aag atc agg caa cta ttg 2203
Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu Leu
90 95 100

tgg ttt cat ata tct tgc ctt act ttt gga aga gag act gta ctt gaa 2251
Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu Glu
105 110 115

tat ttg gtc tct ttc gga gtg tgg att cgc act cct cca gcc tat aga 2299
Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg
120 125 130

cca cca aat gcc cct atc tta tca aca ctt ccg gaa act act gtt gtt 2347
Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val
135 140 145

aga cga cgg gac cga ggc agg tcc cct aga aga aga act ccc tcg cct 2395
Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
150 155 160 165

cgc aga cgc aga tct caa tcg ccg cgt cgc aga aga tct caa tct cgg 2443
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
170 175 180

gaa tct caa tgt tag tattccttgg actcataagg tgggaaacct tactgggctt 2498
Glu Ser Gln Cys
185

tattcctcta cagtagccat cttaatcct gaatggcaaa ctccttcctt tcctaagatt 2558
catttacaag aggacattat tgataggtgt caacaatttg tggccctct cactgtaaat 2618
gaaaagagaa gattgaaatt aattatgcct gctagattct atcctaccca cactaaatat 2678

ttgcccttag acaaaggaat taaaccttat tatccagatc aggtagttaa tcattacttc 2738
caaaccagac attatttaca tactcttgg aaggctggta ttctatataa gagggaaacc 2798

acacgtagcg catcatttg cggtcacca tattcttggg aacaagagct acagcatggg 2858

aggttggtca ttaaaacctc gcaaaggcat gggacgaat ctttctgttc ccaaccctct 2918

gggattctt cccgatcatc agttggaccc tgcattcgga gccaactcaa acaatccaga 2978

ttgggacttc aacccatca aggaccactg gccagcagcc aaccaggtag gagtgggagc 3038

attcgggcca gggctcaccc ctccacacgg cggtatatttgg ggtggagcc ctcaggctca 3098

ggccatattg accacagtgt caacaattcc tcctcctgcc tccaccaatc ggcagtcagg 3158

aaggcagcct actccatct ctccacctct aagagacagt catcctcagg ccatgcagtg 3218

gaa 3221

<210> 134
<211> 185
<212> PRT
<213> Hepatitis B virus

<400> 134
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
65 70 75 80
Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu Thr Thr Val Val Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg
145 150 155 160
Arg Thr Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
165 170 175
Arg Ser Gln Ser Arg Glu Ser Gln Cys
180 185

<210> 135
<211> 188
<212> PRT
<213> Woodchuck hepatitis B virus

<400> 135
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu
1 5 10 15

Asn Phe Leu Pro Leu Asp Phe Pro Asp Leu Asn Ala Leu Val Asp
20 25 30

Thr Ala Thr Ala Leu Tyr Glu Glu Leu Thr Gly Arg Glu His Cys
35 40 45

Ser Pro His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Asp Glu
50 55 60

Leu Thr Lys Leu Ile Ala Trp Met Ser Ser Asn Ile Thr Ser Glu Gln
65 70 75 80

Val Arg Thr Ile Ile Val Asn His Val Asn Asp Thr Trp Gly Leu Lys
85 90 95

Val Arg Gln Ser Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln
100 105 110

His Thr Val Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Ala Pro Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu His Thr Val Ile Arg Arg Arg Gly Gly Ala Arg Ala Ser Arg Ser
145 150 155 160

Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro
165 170 175

Arg Arg Arg Arg Ser Gln Ser Pro Ser Thr Asn Cys
180 185

<210> 136
<211> 217
<212> PRT
<213> Ground squirrel hepatitis virus

<400> 136
Met Tyr Leu Phe His Leu Cys Leu Val Phe Ala Cys Val Pro Cys Pro
1 5 10 15

Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp
20 25 30

Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu Asn Phe
35 40 45

Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp Thr Ala
50 55 60

Ala Ala Leu Tyr Glu Glu Leu Thr Gly Arg Glu His Cys Ser Pro
65 70 75 80

His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Glu Glu Leu Thr
85 90 95

Arg Leu Ile Thr Trp Met Ser Glu Asn Thr Thr Glu Glu Val Arg Arg
100 105 110

Ile Ile Val Asp His Val Asn Asn Thr Trp Gly Leu Lys Val Arg Gln
115 120 125

Thr Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln His Thr Val
130 135 140

Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Ala Pro
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu His Thr
165 170 175

Val Ile Arg Arg Arg Gly Gly Ser Arg Ala Ala Arg Ser Pro Arg Arg
180 185 190

Arg Thr Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
195 200 205

Arg Ser Gln Ser Pro Ala Ser Asn Cys
210 215

<210> 137

<211> 262

<212> PRT

<213> Snow Goose Hepatitis B Virus

<400> 137

Met Asp Val Asn Ala Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro
1 5 10 15

Asp Asp Phe Phe Pro Lys Ile Glu Asp Leu Val Arg Asp Ala Lys Asp
20 25 30

Ala Leu Glu Pro Tyr Trp Lys Ser Asp Ser Ile Lys Lys His Val Leu
35 40 45

Ile Ala Thr His Phe Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr
50 55 60

Gln Gly Met His Glu Ile Ala Glu Ala Ile Arg Ala Val Ile Pro Pro
65 70 75 80

Thr Thr Ala Pro Val Pro Ser Gly Tyr Leu Ile Gln His Asp Glu Ala
85 90 95

Glu Glu Ile Pro Leu Gly Asp Leu Phe Lys Glu Gln Glu Glu Arg Ile
100 105 110

Val Ser Phe Gln Pro Asp Tyr Pro Ile Thr Ala Arg Ile His Ala His
115 120 125

Leu Lys Ala Tyr Ala Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg
130 135 140

Arg Leu Leu Trp Trp His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Thr
145 150 155 160

Val Thr Asn Tyr Ile Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu
165 170 175

Lys Tyr Arg Gly Arg Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro
180 185 190

Ile Gln Val Ala Gln Gly Gly Arg Lys Thr Ser Thr Ala Thr Arg Lys
195 200 205

Pro Arg Gly Leu Glu Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val
210 215 220

Tyr Gly Arg Arg Arg Ser Lys Ser Arg Glu Arg Arg Ala Ser Ser Pro
225 230 235 240

Gln Arg Ala Gly Ser Pro Leu Pro Arg Ser Ser Ser Ser His His Arg
245 250 255

Ser Pro Ser Pro Arg Lys
260

<210> 138

<211> 305

<212> PRT

<213> Duck hepatitis B virus

<400> 138

Met Trp Asp Leu Arg Leu His Pro Ser Pro Phe Gly Ala Ala Cys Gln
1 5 10 15

Gly Ile Phe Thr Ser Ser Leu Leu Phe Leu Val Thr Val Pro Leu
20 25 30

Val Cys Thr Ile Val Tyr Asp Ser Cys Leu Cys Met Asp Ile Asn Ala
35 40 45

Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro
50 55 60

Lys Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr
65 70 75 80

Trp Arg Asn Asp Ser Ile Lys Lys His Val Leu Ile Ala Thr His Phe
85 90 95

Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met His Glu
100 105 110

Ile Ala Glu Ala Leu Arg Ala Ile Ile Pro Ala Thr Thr Ala Pro Val
115 120 125

Pro Gln Gly Phe Leu Val Gln His Glu Glu Ala Glu Glu Ile Pro Leu
130 135 140

Gly Glu Leu Phe Arg Tyr Gln Glu Glu Arg Leu Thr Asn Phe Gln Pro
145 150 155 160

Asp Tyr Pro Val Thr Ala Arg Ile His Ala His Leu Lys Ala Tyr Ala
165 170 175

Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg Arg Leu Leu Trp Trp
180 185 190

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His Tyr Asn Cys Leu Leu Trp Gly Glu Pro Asn Val Thr Asn Tyr Ile
195 200 205

Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Lys
210 215 220

Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln
225 230 235 240

Gly Gly Arg Asn Lys Thr Gln Gly Val Arg Lys Ser Arg Gly Leu Glu
245 250 255

Pro Arg Arg Arg Val Lys Thr Thr Ile Val Tyr Gly Arg Arg Arg
260 265 270

Ser Lys Ser Arg Glu Arg Arg Ala Pro Thr Pro Gln Arg Ala Gly Ser
275 280 285

Pro Leu Pro Arg Thr Ser Arg Asp His His Arg Ser Pro Ser Pro Arg
290 295 300

Glu
305

<210> 139

<211> 212

<212> PRT

<213> Haemophilus influenzae

<400> 139

Met Lys Lys Thr Leu Leu Gly Ser Leu Ile Leu Leu Ala Phe Ala Gly
1 5 10 15

Asn Val Gln Ala Ala Ala Asn Ala Asp Thr Ser Gly Thr Val Thr Phe
20 25 30

Phe Gly Lys Val Val Glu Asn Thr Cys Gln Val Asn Gln Asp Ser Glu
35 40 45

Tyr Glu Cys Asn Leu Asn Asp Val Gly Lys Asn His Leu Ser Gln Gln
50 55 60

Gly Tyr Thr Ala Met Gln Thr Pro Phe Thr Ile Thr Leu Glu Asn Cys
65 70 75 80

Asn Val Thr Thr Asn Asn Lys Pro Lys Ala Thr Lys Val Gly Val
85 90 95

Tyr Phe Tyr Ser Trp Glu Ile Ala Asp Lys Asp Asn Lys Tyr Thr Leu
100 105 110

Lys Asn Ile Lys Glu Asn Thr Gly Thr Asn Asp Ser Ala Asn Lys Val
115 120 125

Asn Ile Gln Leu Leu Glu Asp Asn Gly Thr Ala Glu Ile Lys Val Val
130 135 140

Gly Lys Thr Thr Asp Phe Thr Ser Glu Asn His Asn Gly Ala Gly
145 150 155 160

Ala Asp Pro Val Ala Thr Asn Lys His Ile Ser Ser Leu Thr Pro Leu
165 170 175

Asn Asn Gln Asn Ser Ile Asn Leu His Tyr Ile Ala Gln Tyr Tyr Ala
180 185 190

Thr Gly Val Ala Glu Ala Gly Lys Val Pro Ser Ser Val Asn Ser Gln
195 200 205

Ile Ala Tyr Glu
210

<210> 140
<211> 139
<212> PRT
<213> Pseudomonas stutzeri

<400> 140
Met Lys Ala Gln Met Gln Lys Gly Phe Thr Leu Ile Glu Leu Met Ile
1 5 10 15

Val Val Ala Ile Ile Gly Ile Leu Ala Ala Ile Ala Leu Pro Ala Tyr
20 25 30

Gln Asp Tyr Thr Val Arg Ser Asn Ala Ala Ala Ala Leu Ala Glu Ile
35 40 45

Thr Pro Gly Lys Ile Gly Phe Glu Gln Ala Ile Asn Glu Gly Lys Thr
50 55 60

Pro Ser Leu Thr Ser Thr Asp Glu Gly Tyr Ile Gly Ile Thr Asp Ser
65 70 75 80

Thr Ser Tyr Cys Asp Val Asp Leu Asp Thr Ala Ala Asp Gly His Ile
85 90 95

Glu Cys Thr Ala Lys Gly Gly Asn Ala Gly Lys Phe Asp Gly Lys Thr
100 105 110

Ile Thr Leu Asn Arg Thr Ala Asp Gly Glu Trp Ser Cys Ala Ser Thr
115 120 125

Leu Asp Ala Lys Tyr Lys Pro Gly Lys Cys Ser
130 135

<210> 141
<211> 59
<212> PRT
<213> Caulobacter crescentus

<400> 141
Met Thr Lys Phe Val Thr Arg Phe Leu Lys Asp Glu Ser Gly Ala Thr
1 5 10 15

Ala Ile Glu Tyr Gly Leu Ile Val Ala Leu Ile Ala Val Val Ile Val
20 25 30

Thr Ala Val Thr Thr Leu Gly Thr Asn Leu Arg Thr Ala Phe Thr Lys
35 40 45

Ala Gly Ala Ala Val Ser Thr Ala Ala Gly Thr
50 55

<210> 142
<211> 173
<212> PRT
<213> Escherichia coli

<400> 142
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
1 5 10 15

Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
20 25 30
Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
35 40 45

Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
50 55 60

Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn
65 70 75 80

Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
85 90 95

Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
100 105 110

Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
115 120 125

Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
130 135 140

Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
145 150 155 160

Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
165 170

<210> 143
<211> 173
<212> PRT
<213> Escherichia coli

<400> 143
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
1 5 10 15

Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
20 25 30
Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
35 40 45

Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
50 55 60

Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn
65 70 75 80

Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
85 90 95

Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
100 105 110

Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
115 120 125

Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
130 135 140

Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
145 150 155 160

Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
165 170

<210> 144
<211> 172
<212> PRT
<213> Escherichia coli

<400> 144
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Thr Pro Gln
1 5 10 15

Gly Gln Gly Arg Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
20 25 30

Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
35 40 45

Ser Lys Ser Phe Leu Ala Asn Asp Gly Gln Ser Lys Pro Met Asn Leu
50 55 60

Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Asn Gly Asn
65 70 75 80

Ala Lys Thr Gly Ser Val Lys Leu Ala Phe Thr Gly Pro Thr Val Ser
85 90 95

Gly His Pro Ser Glu Leu Ala Thr Asn Gly Gly Pro Gly Thr Ala Ile
100 105 110

Met Ile Gln Ala Ala Gly Lys Asn Val Pro Phe Asp Gly Thr Glu Gly
115 120 125

Asp Pro Asn Leu Leu Lys Asp Gly Asp Asn Val Leu His Tyr Thr Thr
130 135 140

Val Gly Lys Lys Ser Ser Asp Gly Asn Ala Gln Ile Thr Glu Gly Ala
145 150 155 160

Phe Ser Gly Val Ala Thr Phe Asn Leu Ser Tyr Gln
165 170

<210> 145
<211> 853
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (281)..(829)

<400> 145
acgtttctgt ggctcgacgc atttcctca ttcttctctc caaaaaccac ctcatgcaat 60
ataaaacatct ataaataaaag ataacaataa gaatattaag ccaacaaata aactgaaaaa 120
gttgcgtccgc gatgcattac ctctatgagt caaaaatggcc ccaatgttc atctttggg 180
ggaaaactgtg cagtgttggc agtcaaactc gttgacaaac aaagtgtaca gaacgactgc 240
ccatgtcgat ttagaaatag tttttgaaa ggaaaggcgc atg aaa att aaa act 295
Met Lys Ile Lys Thr
1 5
ctg gca atc gtt gtt ctg tcg gct ctg tcc ctc agt tct acg acg gct 343
Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu Ser Thr Thr Ala
10 15 20
ctg gcc gct gcc acg acg gtt aat ggt ggg acc gtt cac ttt aaa ggg 391
Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr Val His Phe Lys Gly
25 30 35
gaa gtt gtt aac gcc gct tgc gca gtt gat gca ggc tct gtt gat caa 439
Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala Gly Ser Val Asp Gln
40 45 50
acc gtt cag tta gga cag gtt cgt acc gca tcg ctg gca cag gaa gga 487
Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser Leu Ala Gln Glu Gly
55 60 65
gca acc agt tct gtc ggt ttt aac att cag ctg aat gat tgc gat 535
Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln Leu Asn Asp Cys Asp
70 75 80 85
acc aat gtt gca tct aaa gcc gct gtt gcc ttt tta ggt acg gcg att 583
Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe Leu Gly Thr Ala Ile
90 95 100
gat gcg ggt cat acc aac gtt ctg gct ctg cag agt tca gct gcg ggt 631
Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln Ser Ser Ala Ala Gly
105 110 115
agc gca aca aac gtt ggt gtg cag atc ctg gac aga acg ggt gct gcg 679
Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp Arg Thr Gly Ala Ala
120 125 130
ctg acg ctg gat ggt gcg aca ttt agt tca gaa aca acc ctg aat aac 727
Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu Thr Thr Leu Asn Asn
135 140 145
gga acc aat acc att ccg ttc cag gcg cgt tat ttt gca acc ggg gcc 775
Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr Phe Ala Thr Gly Ala
150 155 160 165
gca acc ccg ggt gct gct aat gcg gat gcg acc ttc aag gtt cag tat 823
Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe Lys Val Gln Tyr
170 175 180
caa taa cctacctagg ttcagggacg ttca 853
Gln

<210> 146
<211> 182
<212> PRT

<213> Escherichia coli

<400> 146
Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
1 5 10 15
Ser Ser Thr Thr Ala Leu Ala Ala Thr Thr Val Asn Gly Gly Thr
20 25 30
Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
35 40 45
Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
50 55 60
Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65 70 75 80
Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
85 90 95
Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
100 105 110
Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
115 120 125
Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
130 135 140
Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145 150 155 160
Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
165 170 175
Phe Lys Val Gln Tyr Gln
180

<210> 147

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG peptide

<400> 147

Cys Gly Gly Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

<210> 148

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 148

ccggattca tggacattga cccttataaaa g

31

<210> 149

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 149
gtgcagtatg gtgaggtgag gaatgctcag gagactc 37

<210> 150
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 150
gsgtctcctg agcattcctc acctcaccat actgcac 37

<210> 151
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 151
cttccaaaag tgagggaaaga aatgtgaaac cac 33

<210> 152
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 152
cgcgtcccaa gcttctaaac aacagtagtc tccggaagcg ttgatacg 47

<210> 153
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 153
gtggtttcac atttcttccc tcactttgg aag 33

<210> 154
<211> 281
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 154
Met Ser Glu Tyr Gln Pro Ser Leu Phe Ala Leu Asn Pro Met Gly Phe
1 5 10 15

Ser Pro Leu Asp Gly Ser Lys Ser Thr Asn Glu Asn Val Ser Ala Ser
20 25 30

Thr Ser Thr Ala Lys Pro Met Val Gly Gln Leu Ile Phe Asp Lys Phe
35 40 45

Ile Lys Thr Glu Glu Asp Pro Ile Ile Lys Gln Asp Thr Pro Ser Asn
50 55 60

Leu Asp Phe Asp Phe Ala Leu Pro Gln Thr Ala Thr Ala Pro Asp Ala
65 70 75 80

Lys Thr Val Leu Pro Ile Pro Glu Leu Asp Asp Ala Val Val Glu Ser
85 90 95

Phe Phe Ser Ser Ser Thr Asp Ser Thr Pro Met Phe Glu Tyr Glu Asn
100 105 110

Leu Glu Asp Asn Ser Lys Glu Trp Thr Ser Leu Phe Asp Asn Asp Ile
115 120 125

Pro Val Thr Thr Asp Asp Val Ser Leu Ala Asp Lys Ala Ile Glu Ser
130 135 140

Thr Glu Glu Val Ser Leu Val Pro Ser Asn Leu Glu Val Ser Thr Thr
145 150 155 160

Ser Phe Leu Pro Thr Pro Val Leu Glu Asp Ala Lys Leu Thr Gln Thr
165 170 175

Arg Lys Val Lys Lys Pro Asn Ser Val Val Lys Lys Ser His His Val
180 185 190

Gly Lys Asp Asp Glu Ser Arg Leu Asp His Leu Gly Val Val Ala Tyr
195 200 205

Asn Arg Lys Gln Arg Ser Ile Pro Leu Ser Pro Ile Val Pro Glu Ser
210 215 220

Ser Asp Pro Ala Ala Leu Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg
225 230 235 240

Arg Ser Arg Ala Arg Lys Leu Gln Arg Met Lys Gln Leu Glu Asp Lys
245 250 255

Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala
260 265 270

Arg Leu Lys Lys Leu Val Gly Glu Arg
275 280

<210> 155
<211> 181
<212> PRT
<213> Escherichia coli

<400> 155
Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
1 5 10 15

Ser Ser Thr Ala Ala Leu Ala Ala Thr Thr Val Asn Gly Gly Thr
20 25 30

Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
35 40 45.

Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
50 55 60

Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65 70 75 80

Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
85 90 95

Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
100 105 110

Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
115 120 125

Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
130 135 140

Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145 150 155 160

Phe Ala Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe
165 170 175

Lys Val Gln Tyr Gln
180

<210> 156

<211> 447

<212> DNA

<213> Hepatitis B

<220>

<221> CDS

<222> (1)..(447)

<400> 156

atg gac att gac cct tat aaa gaa ttt gga gct act gtg gag tta ctc 48
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

tcg ttt ttg cct tct gac ttc ttt cct tcc gta cga gat ctt cta gat 96
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

acc gcc gca gct ctg tat cgg gat gcc tta gag tct cct gag cat tgt 144
Thr Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

tca cct cac cat act gca ctc agg caa gca att ctt tgc tgg gga gac 192
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

tta atg act cta gct acc tgg gtg ggt act aat tta gaa gat cca gca 240
Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala
65 70 75 80

tct agg gac cta gta gtc agt tat gtc aac act aat gtg ggc cta aag 288
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
85 90 95

ttc aga caa tta ttg tgg ttt cac att tct tgt ctc act ttt gga aga 336
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg

DRAFT PROPOSED CODE

100 105 110

gaa acg gtt cta gag tat ttg gtc tct ttt gga gtg tgg att cgc act 384
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

cct cca gcc tat aga cca cca aat gcc cct atc cta tca acg ctt ccg 432
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

gag act act gtt gtt 447
Glu Thr Thr Val Val
145

<210> 157
<211> 149
<212> PRT
<213> Hepatitis B

<400> 157
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val
145

<210> 158
<211> 152
<212> PRT
<213> Hepatitis B

<400> 158
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp

BDBTQD"293090BT

20 25 30

Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Gly Gly
65 70 75 80

Lys Gly Gly Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val
85 90 95

Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr
100 105 110

Phe Gly Arg Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp
115 120 125

Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser
130 135 140

Thr Leu Pro Glu Thr Thr Val Val
145 150

<210> 159
<211> 132
<212> PRT
<213> Bacteriophage Q Beta

<400> 159
Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Lys
1 5 10 15

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
20 25 30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
35 40 45

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
50 55 60

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
65 70 75 80

Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser Phe
85 90 95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
100 105 110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
115 120 125

Asn Pro Ala Tyr
130

<210> 160
<211> 129
<212> PRT

<213> Bacteriophage R 17

<400> 160

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
1 5 10 15

Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
20 25 30

Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
35 40 45

Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
50 55 60

Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65 70 75 80

Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala
85 90 95

Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
100 105 110

Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
115 120 125

Tyr

<210> 161

<211> 130

<212> PRT

<213> Bacteriophage fr

<400> 161

Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15

Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45

Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
50 55 60

Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val
65 70 75 80

Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
85 90 95

Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr
100 105 110

Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr
130

<210> 162
<211> 130
<212> PRT
<213> Bacteriophage GA

<400> 162

Met Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly
1 5 10 15

Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp
20 25 30

Leu Ser Asn Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr
35 40 45

Arg Ala Ser Gly Ala Asp Lys Arg Lys Tyr Ala Ile Lys Leu Glu Val
50 55 60

Pro Lys Ile Val Thr Gln Val Val Asn Gly Val Glu Leu Pro Gly Ser
65 70 75 80

Ala Trp Lys Ala Tyr Ala Ser Ile Asp Leu Thr Ile Pro Ile Phe Ala
85 90 95

Ala Thr Asp Asp Val Thr Val Ile Ser Lys Ser Leu Ala Gly Leu Phe
100 105 110

Lys Val Gly Asn Pro Ile Ala Glu Ala Ile Ser Ser Gln Ser Gly Phe
115 120 125

Tyr Ala
130

<210> 163
<211> 132
<212> PRT
<213> Bacteriophage SP

<400> 163

Met Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly
1 5 10 15

Asp Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys
50 55 60

Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys
65 70 75 80

Asp Pro Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe
85 90 95

Thr Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu
100 105 110

Ala Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu
115 120 125

Asn Pro Ala Tyr
130

<210> 164
<211> 130
<212> PRT
<213> Bacteriophage MS2

<400> 164

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 . 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
115 120 125

Ile Tyr
130

<210> 165
<211> 133
<212> PRT
<213> Bacteriophage M11

<400> 165
Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Lys Gly
1 5 10 15

Asp Val Thr Leu Asp Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ser Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Val Glu Glu Arg Ala Leu Val Arg Thr Glu
100 105 110

Leu Gln Ala Leu Leu Ala Asp Pro Met Leu Val Asn Ala Ile Asp Asn
115 120 125

Leu Asn Pro Ala Tyr
130

<210> 166
<211> 133
<212> PRT
<213> Bacteriophage MX1

<400> 166
Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Asn Gly
1 5 10 15

Asp Val Thr Leu Asn Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ala Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Leu Val Arg Thr Glu
100 105 110

Leu Lys Ala Leu Leu Ala Asp Pro Met Leu Ile Asp Ala Ile Asp Asn
115 120 125

Leu Asn Pro Ala Tyr
130

<210> 167
<211> 330
<212> PRT
<213> Bacteriophage NL95

<400> 167
Met Ala Lys Leu Asn Lys Val Thr Leu Thr Gly Ile Gly Lys Ala Gly
1 5 10 15

Asn Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly

	20	25	30
Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg			
35	40		45
Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys			
50	55		60
Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Lys Asp Ala Cys			
65	70	75	80
Asp Pro Ser Val Thr Arg Ser Gly Ser Arg Asp Val Thr Leu Ser Phe			
85	90		95
Thr Ser Tyr Ser Thr Glu Arg Glu Arg Ala Leu Ile Arg Thr Glu Leu			
100	105		110
Ala Ala Leu Leu Lys Asp Asp Leu Ile Val Asp Ala Ile Asp Asn Leu			
115	120		125
Asn Pro Ala Tyr Trp Ala Ala Leu Leu Ala Ala Ser Pro Gly Gly Gly			
130	135		140
Asn Asn Pro Tyr Pro Gly Val Pro Asp Ser Pro Asn Val Lys Pro Pro			
145	150	155	160
Gly Gly Thr Gly Thr Tyr Arg Cys Pro Phe Ala Cys Tyr Arg Arg Gly			
165	170		175
Glu Leu Ile Thr Glu Ala Lys Asp Gly Ala Cys Ala Leu Tyr Ala Cys			
180	185		190
Gly Ser Glu Ala Leu Val Glu Phe Glu Tyr Ala Leu Glu Asp Phe Leu			
195	200		205
Gly Asn Glu Phe Trp Arg Asn Trp Asp Gly Arg Leu Ser Lys Tyr Asp			
210	215	220	
Ile Glu Thr His Arg Arg Cys Arg Gly Asn Gly Tyr Val Asp Leu Asp			
225	230	235	240
Ala Ser Val Met Gln Ser Asp Glu Tyr Val Leu Ser Gly Ala Tyr Asp			
245		250	255
Val Val Lys Met Gln Pro Pro Gly Thr Phe Asp Ser Pro Arg Tyr Tyr			
260	265		270
Leu His Leu Met Asp Gly Ile Tyr Val Asp Leu Ala Glu Val Thr Ala			
275	280		285
Tyr Arg Ser Tyr Gly Met Val Ile Gly Phe Trp Thr Asp Ser Lys Ser			
290	295		300
Pro Gln Leu Pro Thr Asp Phe Thr Arg Phe Asn Arg His Asn Cys Pro			
305	310	315	320
Val Gln Thr Val Ile Val Ile Pro Ser Leu			
325		330	

<210> 168

<211> 134

<212> PRT

<213> Apis mellifera

<400> 168
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15

Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30

Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60

Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65 70 75 80

Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95

Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110

Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

Phe Asp Leu Arg Lys Tyr
130

<210> 169

<211> 129

<212> PRT

<213> Apis mellifera

<400> 169
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
1 5 10 15

Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30

Thr His Asp Met Cys Pro Asn Val Met Ser Ala Gly Glu Ser Lys His
35 40 45

Gly Leu Thr Asp Thr Ala Ser Arg Leu Ser Cys Asn Asp Asn Asp Leu
50 55 60

Phe Tyr Lys Asp Ser Ala Asp Thr Ile Ser Ser Tyr Phe Val Gly Lys
65 70 75 80

Met Tyr Phe Asn Leu Ile Asn Thr Lys Cys Tyr Lys Leu Glu His Pro
85 90 95

Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg Cys Leu His Tyr Thr
100 105 110

Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp Phe Asp Leu Arg Lys
115 120 125

Tyr

<210> 170
<211> 134
<212> PRT
<213> Apis dorsata

<400> 170
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
1 5 10 15

Ser Pro Asp Glu Leu Gly Arg Phe Lys His Thr Asp Ser Cys Cys Arg
20 25 30
Ser His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45

Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60

Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ser Asp Thr Ile Ser Ser
65 70 75 80

Tyr Phe Val Gly Glu Met Tyr Phe Asn Ile Leu Asp Thr Lys Cys Tyr
85 90 95

Lys Leu Glu His Pro Val Thr Gly Cys Gly Lys Arg Thr Glu Gly Arg
100 105 110

Cys Leu Asn Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

Phe Asp Leu Arg Lys Tyr
130

<210> 171
<211> 134
<212> PRT
<213> Apis cerana

<400> 171
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
1 5 10 15

Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30

Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45

Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60

Asp Thr Phe Tyr Asp Cys Leu Lys Asn Ser Gly Glu Lys Ile Ser Ser
65 70 75 80

Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95

Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110

Cys Leu Arg Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

Phe Asp Leu Arg Lys Tyr
130

<210> 172
<211> 136
<212> PRT
<213> Bombus pennsylvanicus

<400> 172

Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly Asn Gly Asn Ile Ala Asn
1 5 10 15

Gly Thr Asn Glu Leu Gly Leu Trp Lys Glu Thr Asp Ala Cys Cys Arg
20 25 30

Thr His Asp Met Cys Pro Asp Ile Ile Glu Ala His Gly Ser Lys His
35 40 45

Gly Leu Thr Asn Pro Ala Asp Tyr Thr Arg Leu Asn Cys Glu Cys Asp
50 55 60

Glu Glu Phe Arg His Cys Leu His Asn Ser Gly Asp Ala Val Ser Ala
65 70 75 80

Ala Phe Val Gly Arg Thr Tyr Phe Thr Ile Leu Gly Thr Gln Cys Phe
85 90 95

Arg Leu Asp Tyr Pro Ile Val Lys Cys Lys Val Lys Ser Thr Ile Leu
100 105 110

Arg Glu Cys Lys Glu Tyr Glu Phe Asp Thr Asn Ala Pro Gln Lys Tyr
115 120 125

Gln Trp Phe Asp Val Leu Ser Tyr
130 135

<210> 173
<211> 142
<212> PRT
<213> Heloderma suspectum

<400> 173

Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
1 5 10 15

Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
20 25 30

Cys Arg Asp His Asp His Cys Ser Asp Thr Met Ala Ala Leu Glu Tyr
35 40 45

Lys His Gly Met Arg Asn Tyr Arg Pro His Thr Val Ser His Cys Asp
50 55 60

Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Asn Val Lys Asp Arg Thr
65 70 75 80

Ala Asp Leu Val Gly Met Thr Tyr Phe Thr Val Leu Lys Ile Ser Cys
85 90 95

Phe Glu Leu Glu Glu Gly Glu Cys Val Asp Asn Asn Phe Ser Gln
100 105 110

Gln Cys Thr Lys Ser Glu Ile Met Pro Val Ala Lys Leu Val Ser Ala
115 120 125

Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly
130 135 140

<210> 174

<211> 143

<212> PRT

<213> Heloderma suspectum

<400> 174

Gly Ala Phe Ile Met Pro Gly Thr Leu Trp Cys Gly Ala Gly Asn Ala
1 5 10 15

Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
20 25 30

Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr
35 40 45

Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
50 55 60

Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr
65 70 75 80

Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys
85 90 95

Phe Glu Leu Glu Glu Gly Cys Val Asp Trp Asn Phe Trp Leu
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Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
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Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr

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Asp Ser Tyr Ile His Trp Ile Arg Gln Ala Pro Gly His Gly Leu Glu			
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Trp Val Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Pro			
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Arg Phe Gln Gly Arg Val Thr Met Thr Arg Asp Ala Ser Phe Ser Thr			
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Ala Tyr Met Asp Leu Arg Ser Leu Arg Ser Asp Asp Ser Ala Val Phe			
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Tyr Cys Ala Lys Ser Asp Pro Phe Trp Ser Asp Tyr Tyr Asn Phe Asp			
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Tyr Ser Tyr Thr Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val			
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Ser Ser Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys			
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Cys Lys Asn Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu			
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Ser Leu Asn Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu			
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Tyr Thr Cys Gln Val Thr Tyr Gln Gly His Thr Phe Glu Asp Ser Thr
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Lys Lys Cys Ala Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser
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Cys Leu Val Val Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr
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Trp Ser Arg Ala Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu
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Glu Lys Gln Arg Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val
420 425 430

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His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser
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Gly Pro Arg Ala Ala Pro Glu Val Tyr Ala Phe Ala Thr Pro Glu Trp
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275 280 285

Ala Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly
290 295 300

Ala Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile
305 310 315 320

Gln Ala Val Ile Val Val Pro Arg Ala
325

<210> 218

<211> 770

<212> PRT

<213> Amyloid-Beta Protein (Homo Sapiens)

<400> 218

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg
1 5 10 15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
210 215 220

Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
260 265 270

Ala Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715 720

Val Met Leu Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
770

<210> 219

<211> 82

<212> PRT

<213> Beta-Amyloid Peptide Precursor (Homo Sapiens)

<400> 219

Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys
1 5 10 15

Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln
20 25 30

Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile
35 40 45

Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Ile Ile
50 55 60

Thr Leu Val Met Leu Lys Lys Gln Tyr Thr Ser Asn His His Gly Val
65 70 75 80

Val Glu

<210> 220

<211> 42

<212> PRT

<213> Amyloid Beta Peptide

<400> 220

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40

221:

RANKL_human: TrEMBL:O14788: extracellular domain

YFRAQMDPNRIS EDGTHCIYRI LRLHENADFQ DTTLESQDTK LIPDSCRRRIK QAFQGAVQKE
LQHIVGSQHI RAEKAMVDGS WLDLAKRSKL EAQPFAHLTI NATDIPSGSH KVSLSSWYHD
RGWAKISNMT FSNGKLVNQ DGFYYLYANI CFRHHETSGD LATEYLQLMV YVTKTSIKIP
SSHTLMKGGS TKYWSGNSEF HFYSINVGGF FKLRSGEEIS IEVSNPSLLD PDQDATYFGA FKVRDID

222:

RANKL_human: spliced isoformTrEMBL:O14788

MDPNRISEDG THCIYRILRL HENADFQDTT LESQDTKLIP DSCRRIKQAF QGAVQKELQH
IVGSQHIRAE KAMVDGSWLD LAKRSKLEAQ PFAHLTINAT DIPSGSHKVS LSSWYHDRGW
AKISNMTFSN GKLIVNQDGF YYLYANICFR HHETSGDLAT EYLQLMVYVT KTSIKIPSSH
TLMKGGSTKY WSGNSEFHFY SINVGGFFKL RSGEEISIEV SNPSLLDPDQ DATYFGAFKV
RDID

223:

RANKL_mouse: TrEMBL:O35235: extracellular domain

YFRAQMDPNRI SEDSTHCFYR ILRLHENAGL QDSTLESEDAT LPDSCRRMKQ AFQGAVQKEL
QHIVGPQRFS GAPAMMEGSW LDVAQRGKPE AQPFAHLTIN AASIPSGSHK VTLSSWYHDR

GWAKISNMTL SNGKLRVNQD GFYYLYANIC FRHETSGSV PTDYLQLMVY VVKTSIKIPS
SHNLMKGGST KNWSGNSEFH FYSINVGGFF KLRAFEEISI QVSNPSLLDP DQDATYFGAF KVQDID

224:

RANKL_mouse spliced isoforms: TrEMBL:Q9JJK8

MKQAFQGAVQ KELQHIVGPQ RFSGAPAMME GSWLDVAQRG KPEAQPF AHL TINAASIPSG
SHKVTLSSWY HDRGWAKISN MTLSNGKLRV NQDGFYLYA NICFRHHETS GSVPTDYLQL
MVYVVKTSIK IPSSHNLMKG GSTKNWSGNS EFHFYSINVG GFFKLRAFEE ISIQVSNPSL
LDPDQDATYF GAFKVQDID

225:

MIF_rat: SwissProt

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTSDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYD MNAANVGWNG STFA

226:

MIF_mouse: SwissProt

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTNDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYD MNAANVGWNG STFA

227:

MIF_human: SwissProt

PMFIVNTNVP RASVPGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRNYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFA

228:

Human IL-17

ACCESSION #: AAC50341

1 mtpgktslvs 11111sleai vkagitiprn pgcpnsedkn fprtvmvnln ihnrrntntnp
61 krssdyynrs tspwnlhrne dperypsviw eakcrhlgci nadgnvdyhm nsvpiqqeil
121 vlrrepphcp nsfrlekilv svgctcvtpi vhhva

229:

Mouse IL-17

ACCESSION #: AAA37490

1 mspgrassvs lmlllls1a atvkaaaiip qssacpntea kdf1qnvkvn lkfnslgak
61 vssrrpsdyl nrstspwtlh rnedpdryps viweaqcrhq rcvnaegkld hhmnsvliqq
121 eilvlkrepe scpftrvek mlvgvgctcv asivrqaa

230:

Human IL-13 (precursor)

MALLTTVIALTCLGGFASPGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSG
CSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFN

231:

Human IL-13 (processed)

GPVPPSTALR ELIEELVNIT QNQKAPLCNG SMVWSINLTA
GMYCAALESL INVSGCSAIE KTQRMLSGFC PHKVSAGQFS SLHVRDTKIE VAQFVKDLLL
HLKKLFREGR FN

232:

Mouse IL-13 (processed)

GPVPRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSLTLISNCNAIYRTQRILHGLCNR
KAPTTVSSL PDTKIEVAHFITKLLSYTKQLFRHGPF

233:

Human IL-5 (precursor)

MRMLLHLSLL ALGAAYVYAI PTEIPTSLV KETLALLSTH RTLLIANETL RIPPVVKNH
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQEFLGVMNTEW
IIES

234:

Human IL-5 (processed)

I PTEIPTSLV KETLALLSTH RTLLIANETL RIPPVVKNH
QLCTEEIFQG IGTLESQTVQ GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQ
EFLGVMNTEW IIES

235:

Mouse IL-5 (processed)

MEIPMSTVVKETLTQLSAHRALLTSNETMRLPVPTHKNHQLCIGEIFQQLDILKNQTVRGGTVELFQNLSLIKK
YIDRKKEKCGEERRTRQFLDYLQEFLGVMSTEWAMEG

236:

CCL21 Swissprot: SY21_human: Sequence after cleavage of signal peptide:
SDGGAQD CCLKYSQRKI PAKVVRSYRK QEPSLGCSIP AILFLPRKRS QAELCDPKE LWVQQLMQHL
DKTPSPQKPA QGCRKDRGAS KTGKKGKGSK GCKRTERSQT PKGP

237:

CCL21 Swissprot: SY21_mouse: Sequence after cleavage of signal peptide:
SDGGGQD CCLKYSQKKI PYSTIVRGYRK QEPSLGCPIP AILFSPRKHS KPELCANPEE GWVQNLMRRL

DQPPAPGKQS PGCRKNRGTS KSGKKKGSK GCKRTEQTQP SRG

238:

Swissprot: SDF1_human: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHVA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNKR FKM

239:

Swissprot: SDF1_mouse: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHIA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNK

240:

BLC Sequences: Human: Accession: NP_006410

Amino acids 1-22 are signal peptide.

MKFISTSLLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFIPRRFIDR IQILPRGNNGC
PRKEIIIWKK NKSIVCVDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP

241:

BLC Sequence Mouse: accession: NP_061354

Amino acids 1-21 are signal peptide

MRLSTATLLL LLASCLSPGH GILEAHYTNL KCRCSGVIST VVGLNIIDRI QVTPPGNNGCP
KTEVVIWTKM KKVICVNPR A KWLQRLLRH V QSKSLSSTPQ APVSKRRAA

242:

Human Eotaxin-1

1-23 is Signal peptide

1 mkvsallwl lliaafspq glagpasvpt tccfnlanrk iplqrlesyr ritsgkcpqk
61 avifktklak dicadpkkw vqdsmkyldq ksptpkp

243:

Human Eotaxin-2

1-26 is Signal peptide

1 maglmtivts llflgvcahh iiptgsvvip spccmffvsk ripenrvvsvy qlssrstclk
61 agvifttkkg qqfcgdpkqe wvqrymknl akqkkaspra ravavkgpvq rypgnqtcc

244:

Human Eotaxin-3

1-23 is signal peptide

1 mmglslasav llasllslhl gtatrgsdis ktccfqyshk plpwtwvrsy eftsnscsqr
61 avifttkrgk kvcthprkkw vqkyisllkt pkql

245:

Mouse Eotaxin-1

1-23 is signal peptide

1 mqsstallf1 lltvtsftsq vlahpgsipt sccfimtskk ipntllksyk ritnnrctlk
61 aivfktrlgk eicadpkkkw vqdatkhldq klqtpkp

246:

Mouse Eotaxin-2

1-25 is signal peptide

1 magsativag llllvacacc ifpidsvtip sscctsfisk kipenrvvsy qlangsicpk
61 agvifitkgg hkictdpkll wvqrhiqkld akknqpskga kavrtrkfavq rrrgnstev

247:

M-CSF Sequence: human: the construct would be an N-terminal fragment consisting of residue 33 -181 or 33 –185, corresponding to the soluble form of the receptor.

Accession: NP_000748

MTAPGAAGRC PPTTWLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLIDSQME
TSCQITFEFV DQEQLKDPVC YLKKAFLLVQ DIMEDTMRFR DNTPNAIAIV QLQELSLRK
SCFTKDYEEL DKACVRTFYE TPLQLLEKVK NVFNETKNLL DKDWNIFSKN CNNSFAECSS
QDVVTKPDCN CLYPKAIPSS DPASVSPHQD LAPSMAPVAG LTWEDSEGTE GSSLLPGEQP
LHTVDPGSAK QRPPRSTCQS FEPPETPVVK DSTIGGSPQP RPSVGAFNPG MEDILDSAMG
TNWVPEEASG EASEIPVPQG TELSPSRPGG GSMQTEPARP SNFLSASSPL PASAKGQQPA
DVTGTALPRV GPVRPTGQDW NHTPQKTDHP SALLRDPPEP GSPIRSSPRP QGLSNPSTLS
AQPQLSRSHS SGSVLPLGEL EGRRSTRDRR SPAEPEGGPA SEGAARPLPR FNSVPLTDTH
ERQSEGSSSSP QLQESVFHLL VPSVILVLLA VGGLLFYRWR RRSHQEPQRA DSPLEQPEGS
PLTQDDRQVE LPV

248:

M-CSF Mouse sequence: Mature sequence starts at amino acid 33. Accession.
NP_031804

MTARGAAGRC PSSTWLGSRL LLVCLLMSRS IAKEVSEHCS HMIGNGHLKV LQQLIDSQME
TSCQIAFEFV DQEQLDDPVC YLKKAFFLVQ DIIDETMRFK DNTPNANATE RLQELSNNLN
SCFTKDYEEL NKACVRTFHE TPLQLLEKIK NFFNETKNLL EKDWNIFTKN CNNSFAKCSS
RDVVTKPDCN CLYPKATPSS DPASASPHQD PAPSMAPLAG LAWDDDSQRTE GSSLLPSELP
LRIEDPGSAK QRPPRSTCQT LESTEQPNHG DRLTEDSQPH PSAGGPVPGV EDILESSLGT
NWVLEEASGE ASEGFQTLQEA KFSPSTPVGG SIQAETDRPR ALSASPFPKS TEDQKPVDT

DRPLTEVNPM RPIGQTQNNT PEKTDGTSTL REDHQEPGSP HIATPNPQRV SNSATPVAQL
LLPKSHSWGI VLPLGELEGK RSTRDRRSPA ELEGGSASEG AARPVARFNS I PLTDTGHVE
QHEGSSDPQI PESVFHLLVP GIILVLLTVG GLLFYKWKR SHRDPQTLDS SVGRPEDSSL
TQDEDRQVEL PV

249:

Sequence of Human Resistin: Precursor.

MKALCLLLLVLGLLVSSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSGDLATCPRGFATGCTCG
SACGSWDVRAETTCHCQCAGMDWTGARCCRVQP

250:

Sequence of Mouse Resistin: Precursor.

MKNLSFPLLFLFFLVPELLGSSMPLCPIDEAIDKKIKQDFNSLPNAIKNIGLNCWTSRGKLASCPEGTAVLSCSC
GSACGSWDIREEKVCHCQCARIWTAAARCCKLQVAS

251:

Lymphotoxin- β :

Swissprot: TNFC_human: Sequence of the extracellular domain:

QD QGGLVTETAD PGAQAQQGLG FQKLPEEEPE TDLSPLPAA HLIGAPLKGQ GLGWETTKEQ
AFLTSGTQFS DAEGLALPQD GLYYLYCLVG YRGRAPPGGG DPQGRSVTLR SSLYRAGGAY GPGTPELLLE
GAETVTPVLD PARRQGYGPL WYTSVGFGL VQLRRGERVY VN

252:

Lymphotoxin- β :

Swissprot: TNFC_mouse: Sequence of the extracellular domain:

QD QGRRVEKIIG SGAQAQKRLD DSKPSCILPS PSSLSETPDP RLHPQRSNAS RNLASTSQGP
VAQSSREASA WMТИLSPAAD STPDPGVQQL PKGEPETDLN PELPAAHЛИG AWMSGQGLSW
EASQEEAFLR SGAQFSPHTG LALPQDGVYY LYCHVGYRGR TPPAGRSRAR SLTLRSALYR
AGGAYGRGSP ELLLEGAETV TPVVDPICYG SLWYTSVGFGL GLAQLRSGER VYVNISHPDM
VDYRRGKTFV GAVMVG

253:

RNA-phage PP7:

msktivlsvg eatrtlteiq stadrqifee kvgplvgrlr ltaaslrqnga ktayrvnkl
dqadadvdcast svcgelpkvr ytqvwwshdvt ivansteasr kslydltsl vatsqvedlv
vnlpvplgr

254:

RNA-phage SP A1 protein:

aklnqvtls kigkngdqt1 tltprgvnpt ngvaslseag avpalekrvt vsvaqpsrnr knfkvqiklq nptactrdac dpsvtrsafa dvtlsftsys tdeeralirt elaalladpl ivdaidnlnp aywaallvas sgggdnpsdp dvpvvpdvkp pdgtgrykcp facyrlgsiy evgkegspdi yergdevsvt fdyaledflg ntnwrnwdqr lsdydianrr rcrgngyidl datamqsddf vlsgrgvrk vkfpgafgsi kyllniqgda wldlsevtay rsygmvigfw tdkspqlpt dftqfnanc pvqtviips 1

255:

“Q β 240”:

AKLETVTLGNIGRDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

256:

“Q β 243”:

AKLETVTLGKIGKDQKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

257:

“Q β 250”:

ARLETVTLGNIGRDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

258:

“Q β 259”:

ARLETVTLGNIGKDGRQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

259:

“Q β 251”:

AKLETVTLGNIGKDGRQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

260:

PH19 (SEQ ID NO:260)

TAAGTCCTCTGCCACGTACC

261:

PH20 (SEQ ID NO:261)

TGGAAACCACGCTCACTTCC

262:

PH21 (SEQ ID NO:262)

CGGGATCCGGGATGAAGAACCTTCATTTC

263:

PH22 (SEQ ID NO:263)

GCCTCTAGAGAGGAAGCGACCTGCAGCTTAC

264:

PH29 (SEQ ID NO:264)

CTAGCGGGAGGGGGTGGATGTGGGGACGACTACAAGGATGACGACA

265:

PH30 (SEQ ID NO:265)

AGCTTGTGTCATCCTTGTAGTCGTCCCCACATCCACCCCTCCCG

266:

PH31 (SEQ ID NO:266)

AGCTTACTCACACATGCCACCGTGCCCAGCACCTGAAGCCGAGG

267:

PH32 (SEQ ID NO:267)

CGGCTTCAGGTGCTGGGCACGGTGGGCATGTGTGAGTA

268:

PH35 (SEQ ID NO:268)

CTAGCGGGAGGGGGTGGATGTGGGATCGAAGGTCGCA

269:

PH36 (SEQ ID NO:269)

AGCTTGCGACCTCGATCCCACATCCACCCCTCCG

270:

PH37 (SEQ ID NO:270)

CGGGATCCAGCAGCTGGGCTCGAGGTGCTAGCTTGTAAAC

271:

PH38 (SEQ ID NO:271)

GATCGTTAACAAACAAAGCTAGCACCTCGAGCCCAGCTGGATCCGGTAC

272:

PH39 (SEQ ID NO:272)

CTAGCGGGAGGGGGTGGATGTGGGACGATGACGACA

273:

PH40 (SEQ ID NO:273)

AGCTTGCGTCATCGTCCCCACATCCACCCCTCCG

274:

PH41 (SEQ ID NO:274)

CATGGAGACAGACACACTCCTGCTATGGT

275:

PH42 (SEQ ID NO:275)

GCAGTACCCATAGCAGGAGTGTGTCTGTCTCCATGGTAC

276:

PH43 (SEQ ID NO:276)

ACTGCTGCTCTGGGTCCAGGTTCCACTGGTGACGCG

277:

PH44 (SEQ ID NO:277)

GATCCGCGTCACCACTGGAACCTGGAACCCAGAGCA

278:

SU7 (SEQ ID NO:278)

AGCTTGCGGATCCAGGATATCGGCTCGAGGTTCTAGAGTG

279:

SU8 (SEQ ID NO:279)

GGCCCACTCTAGAACCTCGAGCCGATATCCTGGATCCGCA

280:

Resistin-C-Xa:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARI DWTAARCCKLQVASSLAGGGCGIEGR

281:

Resistin-C-EK

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARI DWTAARCCKLQVASSLAGGGCGDDDD

282:

Resistin-GCG:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARI DWTAARCCKLQVASSLAGGGCG

283:
pCep-Xa-Fc*: (complete sequence)

1	CCCCCGCCGC	CGGACGA	AAACCTGACT	ACGGCATCTC	TGCCCTTCT	TCGCTGGTAC	GAGGAGCGCT
71	TTTGTGTTGT	ATTGGGGCA	GTGCATGAA	TCCCTTCAGT	TGGTGGTAC	AACCTGGCAA	CTGGGCCCTG
141	TTTACCATG	GACACGGGG	GGGACCACAA	ACAAGGGGT	TCTCTGACT	TAGTTGACAT	CCTTATAAAT
211	GGATGTGCA	ATTGGCAAC	ACTGAGTGGC	TTTCATCTG	GAGCAGACTT	TGATGCTGT	GGACTGCAAC
281	ACAAACATTG	CTTTATG	AACCTCTGGC	TGAAGCTCTT	ACACCAATGC	TGGGGACAT	GTACCTCCCA
351	GGGGCCCAGG	AAGACTACGG	GAGGCTACAC	CAACGTCAAT	CAGAGGGCC	TGTGAGCTA	CCGATAAGCG
421	GACCCTAAG	AGGGCATTAG	CAATAGTGT	TATAAGGCC	CCTTGTAA	CCTAACAGGG	TAGCATATGC
491	TTCCCGGTA	GTAGTATATA	CTATCCAGAC	TAACCTAAT	CTAATAGCAT	ATGTTACCCA	ACGGGAAAGCA
561	TATGCTATCG	AATTAGGGT	AGTAAAAGGG	TCTTAAGGAA	CAGCGATATC	TCCCACCCCA	TGAGCTGTCA
631	CGGTTTATT	TACATGGGGT	CAGGATCCA	CGAGGGTAGT	GAACCATTTT	AGTCACAAGG	GCAGTGGCTG
701	AAGATCAAGG	AGCGGGCAGT	GAACCTCTCCT	GAATCTTCGC	CTGCTCTTC	ATTCTCTTC	GTTAGCTAA
771	TAGAATACT	GCTGAGTTGT	GAACAGTAAG	GTGTATGTG	GTTGCTCGAA	AACAAGGTTT	CAGGTGACGC
841	CCCCAGAATA	AAATTGGGAC	GGGGGGTCA	GTGTCGGCAT	TGTGCTATGA	CACCAATATA	ACCTCACAA
911	ACCCCTTGGG	CAATAAACAT	TAGTGTAGGA	ATGAAACATT	CTGAATATCT	TTAACAAATAG	AAATCCATGG
981	GGTGGGGACA	AGCCGTAAAG	ACTGGATGTC	CATCTCACAC	GAATTATGG	CTATGGGCAA	CACATATATCC
1051	TAGTGCAATA	TGATACTGGG	GTATTAAAGA	TGTGTCCTCAG	CGAGGGACCA	AGACAGGTG	ACCATGTTG
1121	TACACTCTAT	TTGTAACAAAG	GGGAAAGAGA	GTGACCGCCG	ACAGCGCGG	ACTCCACTGG	TGTCCTCTAA
1191	CACCCCCCGAA	AATTAAACCG	GGCTCCACGC	CAATGGGCC	CATAAAACAA	GACAAGTGGC	CACTCTTTT
1261	TTGAAATTG	TGGAGTGGGG	GCACGGTCA	GCCCCCACAC	GCGGCCCTGC	GGTTTTGGAC	TGAAAATAA
1331	GGGTGTAATA	ACTTGGCTGA	TTGTAACCCCC	GCTAACCAACT	GCGGTCAAC	CACTTGCCCA	CAAAACACT
1401	AATGGCACCC	CGGGGAATAC	CTGCATTAAGT	AGGTGGGCCG	CGGGAGATAG	GGGCGGATG	GTCGCGATCT
1471	GGAGGACAAA	TTACACACAC	TGGCCTCTGA	GGCCCAAAGG	CAGGGTTGTT	GGTCCTCAT	TTCACGAGGT
1541	CGCTGAGAGC	ACGGTGGGCT	AATGTTGCCA	TGGTAGCAT	ATACTACCCA	AAATATCTGA	TAGCATATGC
1611	TATCCTAAC	TATATCTGGG	TAGCATAGGC	TATCTTAATC	TATATCTGGG	TAGCATATGC	TATCCTAAC
1681	TATATCTGGG	TAGTATATGC	TATCTTAATT	TATATCTGGG	TAGCATAGGC	TATCTTAATC	TATATCTGGG
1751	TAGCATATGC	TATCCTAAC	TATATCTGGG	TAGTATATGC	TATCTTAATC	TGTATCCGGG	TAGCATATGC
1821	TATCCTAAC	GAGATTAGGG	TAGTATATGC	TATCCTAAC	TATATCTGGG	TAGCATATAC	TACCAAATA
1891	TCTGGATAGC	ATATGCTATC	CTAATCTATA	TCTGGGTAGC	ATATGCTATC	CTAATCTATA	TCTGGTAGC
1961	ATAGGCTATC	CTAATCTATA	TCTGGGTAGC	ATATGCTATC	CTAATCTATA	TCTGGGTAGT	ATATGCTATC
2031	CTAATTTATA	TCTGGGTAGC	ATAGGCTATC	CTAATCTATA	TCTGGGTAGC	ATATGCTATC	CTAATCTATA
2101	TCCTGGGTAGT	ATATGCTATC	CTAATCTGT	TCCGGGTAGC	ATATGCTATC	CTCATGCATA	TACAGTCAGC
2171	ATATGATACC	CACTAGTAGA	GTGGGAGTGC	TATCCTTTGC	ATATGCCGCC	ACCTCCCAAG	GGGGCGTGA
2241	TTTTCGCTGC	TTGTCCTTT	CCTGCATGCT	GGTGTCTCCC	ATTCTTAGGT	GAATTTAAGG	AGGCCAGGCT
2311	AAAGCCGTCG	CATGTCGTG	TGCTCACAG	GTAAATGTG	CTAATGTTT	CCAAACGCGAG	AGGTGTTGA
2381	GCGCGGAGCT	GAGTGCAGTC	ACAACATGGG	TATGGCCAAT	TGCCCCCATG	TGGGAGGAGC	AAAATGGTGA
2451	CAAGACAGAT	GGCCAGAAAT	ACACCAACAG	CACCGATGAT	GTCTACTGGG	GATTATTCT	TTAGTGCAGG
2521	GGAATACACG	GCTTTTAATA	CGATTGAGGG	CGTCTCTCAA	CAAGTTACAT	CACTCTGC	CTTCCTCACC
2591	CTCATCTCCA	TCACCTCCCT	CATCTCCGTC	ATCTCCGTC	TCACCTCCG	CGGCAGCCCC	TTCCACCAT
2661	GGTGGAAACC	AGGGAGGCCA	ATCTACTCTCA	TCGTCAGTC	TGACACAGT	CACCCCTGATA	TTGCAAGTAG
2731	GAGCGGGCTT	TGTCATAAAC	AGGTCTTAA	TCGCATCCTT	CAAACACCTCA	TGGCCCATG	GAGTTGTAA
2801	AAAGACCATG	AAATAACAGA	CAATGACTC	CCTTAGCGGG	CGAGGTGTTG	GGCCGGGTCC	AGGGGCCATT
2871	CCAAAGGGGA	GAGCCTCAA	TGGTGTAAAGA	CGACATTGTG	GAATAGCAAG	GGCAGTTCT	CGCCCTTAGGT
2941	TGAAAGGGGA	GGTCTTACTA	CCTCCATATA	CGAACACACC	GGGACCCCAA	GTTCTCTCG	CGGTAGTCT
3011	TTCTACGTG	CTCTTAGC	GGAGAGCTCT	TAAACCTTCT	GCAATGTTCT	CAAATTTCGG	GTTGAAACCT
3081	CCTTGACCAC	GATGCTTCC	AAACCACCC	CCTTTTTG	GCTCTGCTCC	ATCACCTG	CCCCGGGGTC
3151	CACTGCTTGG	GCCTTCTCT	GGGTCTATC	CGGGCCCTG	CTCTATGCTG	CCCCGGGGCA	CCTGCAAGCTC
3221	ACCATCTGGG	CCACCTCTT	GCTGGTATT	AAAAATAATCG	GCTTCCCTA	CAGGGTGGAA	AAATGGCTT
3291	CTACCTGGAG	GGGGCTGCG	CGGTGGAGAC	CGGATGATG	ATGACTGACT	ACTGGGACTC	CTGGCCCTCT
3361	TTTCTCCACG	TCCACGACCT	CTCCCCCTGG	CTCTTCAGC	ACTTCCCCC	CTGGCTCTTT	CACGCTCTCT
3431	ACCCCGGGCG	CCTCTTAC	CTCTCTGACC	CGGCCCTCCA	CTACCTCTC	GACCCGGGCC	TCCACTGCTC
3501	CCTCGACCCCC	GGCCCTCCAC	TCTCTGCTCT	GCCCCCTCTG	CTCCCTGCCC	TCTCTGCTCT	CCTGGCCCTC
3571	CTGCCCCCTCC	TGCTCTGCG	CCTCTGCCCC	CTCTCTGCTCC	TGCCCCCTCT	GCCCCCTCTG	CTCTGCCCC
3641	TCTGCCCCCT	CCTCTGCTC	CTGCCCCCTCC	TGCCCTCTCT	CCTGCTCTG	CCCCCTCTG	CCCTCTGCTG
3711	CCTGCCCCCTC	CTGCCCCCTCC	TGCTCTGCTC	CCTCTGCCCC	CTCTGCTCT	CCCCCTCTG	GCTCTGCCCC
3781	CTCTCTGCTC	TGCCCCCTCT	GCTCTGCCCC	CTCTGCTCT	TGCCCCCTCT	CCCCCTCTG	CTGCCCCCTC
3851	TGCTCTGCTC	CCTCTGCCCC	TGCTCTGCCCC	TCTCTGCTCT	GCCCCCTCT	CTGCTCTG	CCCCCTCTG
3921	CCTCTCTGCC	CTCTCTGCTC	TGCTGCCCC	TCTGCCCCCT	CTCTGCTCT	TGCCCCCTCT	CCTGCTCTG
3991	CCCTCTCTGC	CCCTCTGCTC	CCTCTCTCTG	TCTCTGCCCC	TCTCTGCCCC	CTCTCTGCTC	CTGCCCCCTC
4061	TCTCTGCTCT	GCCCCCTCTG	CCCCCTCTCTG	CCCTCTCTCT	GCTCTGCCCC	CTCTCTGCTC	CTCTGCCCC
4131	CCTGCCCCCTC	CTGCCCCCTC	TGCCCCCTCT	CCTGCTCTG	CCCCCTCTCT	TGCTCTGCTC	CCCCCTCTG
4201	CTGCCCCCTCC	CGCTCTGCTC	CCTGCTCTG	TTCCTACCGTG	GGTCTCTT	CAGCCAATG	AACTGGACG
4271	TTTTGGGGT	CTCCGGACAC	CATCTCTATG	TCTTGGCCCT	GATCTGAGC	CGCCCGGGGC	TCCTGGTCTT
4341	CCGCTCTCTC	GTCTCTGCTC	TCTTCCCCGT	CCTCTGCTCT	GGTTATCACC	CCCTCTCTCT	TGAGGTCAC
4411	TGCGCCCGGA	GCCTCTCTGT	CCAGATGTG	CTCCCTCTCT	TCTCTGCTC	TTCTCCAGGT	CTGTACCTG
4481	CCCCCTGTC	GACATGATTC	ACACTAAAG	AGATCAATAG	ACATCTTAT	TAGACGACG	TCACTGAAATA
4551	CAGGGAGTGC	AGACTCTGC	CCCCCTCCAAC	AGCCCCCCCCA	CCCTCATCCC	CTTCATGGT	GCTGTCAGAC
4621	AGATCCAGGT	CTGAAAATTC	CCCCATCTCC	GAACCATCTCT	CGTCTCTCAT	ACCAATTACT	CGCAGCCCCG
4691	AAAACCTCCG	CTGAACATCC	TCAAGATTG	CGTCTCTGAGC	TCGAAGCCAG	GCCTCAAAATT	CCTGCTCCCC
4761	CTTCTTGTG	GAAGCTGGATT	ATGGGGATT	TCGGGACCC	TCCTCTCTCT	CTTCAGAGTC	ACAGACAGA
4831	GATGCTACTG	GGGCAACCGA	AGAAAAGCTG	GGTGGGGCCT	GTGAGGATCA	GCTTATCGAT	GATAAGCTG

4901 CAAACATGAG AATTCTTGA GACCAAAGGG CCTCGTGATA CGCCTATTT TATAGTTAA TGTCAATGATA
 4971 ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGAA ATGTGCGCGG AACCCCTATT TGTTTATT
 5041 TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA
 5111 AAGGAAGAGT ATGAGTATTG AACATTCCG TGTCGCCCT ATTCCCTTT TTGCGGCATT TTGCCTCCT
 5181 GTTTTGCTC ACCCAGAAC GCTCGTAAA GTAAAAGAT CTGAAGATCA GTTGGGTGCA CGAGTGGTT
 5251 ACATCGAACG GGATCTCAAC AGCGGTAAG TGCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT
 5321 GAGCACTTTT AAAGTCTGC TATGCGGCG GGTATTATCC CGTGTGACG CCGGGCAAGA GCAACTCGGT
 5391 CGCCGCATAC ACTATTCTCA GAATGACTG GTTGAGTACT CACCAAGTCAG AGAAAAGCAT CTTACGGATG
 5461 GCATGACAGT AAAGAGAATTA TGCACTGCTG CCATAACCAG GAGTGAACACT CGTGCAGGCC ACTTACTCT
 5531 GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTG CACAACATGG GGGATCATGT AACTCGCCTT
 5601 GATCGTTGGG AACCGGAGCT GAATGAAGC ATACCAAAACG ACGAGCGTGA CACCAAGATG CCGCAGCAA
 5671 TGGCAACAAC GTTGCAGAAA CTATTAACG GCGAAGTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA
 5741 CTGGATGGAG GCGGATAAAG TTGCAAGGACC ACTTCCTGCG TCAGGCCCTTC CGGCTGGCTG GTTTTATTGCT
 5811 GATAATCTG GAGCCGGTCA GCGGTGATCA TTGAGCAACT GGGGCCAGAT GTGAAGCCCT
 5881 CCCGTATCGT AGTTATCTAC ACGACGGGA GTCAGGCAAC TAGGGATGAA CAAATAGAC AGATCGCTGA
 5951 GATAGGTGCC TCACTGATTA AGCATTGGA ACTGTCAGAC CAAGTTACT CATATATACT TTAGATTGAT
 6021 TAAAAACTTC ATTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTGTA TAATCTCATG ACCAAAATCC
 6091 CTTAACGTGA GTTTTCGTTT CACTGAGCGT CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC
 6161 TTTTTTCTG CGCGTAATCT GCTGCTTGC AAAAAAAA CCACCGCTAC CAGGGTGGGT TTGTTTGC
 6223 GATCAAGAGC TACCAACTCT TTTTCCGAGA GTAACTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC
 6301 TTCTAGTGTG GCCGTAGTTA GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT
 6371 AATCTGTGTA CCACTGGCTG CTGCGAGTGG CGATAAGTC TGTCTTACCG GTTGGACTC AAGACGATAG
 6441 TTACCGATA AGCGCAGCG GTCGGGCTGA ACGGGGGTT CGTGCACAC GCCCAGCTTG GAGCGAACGA
 6511 CCTACACCGA ACTGAGATAC CTACAGCTG AGCTATGAGA AACGGCCACG CTTCAGCGAAG GGAGAAAGC
 6581 GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG CGCACGAGGG AGCTTCCAGG GGGAAACGCC
 6651 TGGTATCTT ATAGTCTGTG CGGGTTTCCG CACCTCTGAC TTGAGCGTCA TTGTTGTGA TGCTCGTCAG
 6721 GGGGGCGGAG CCTATGGAAA AACGCCAGCA AGCGGCCCTT TTACGGGTTT CTGGGCTTTT GCTGCGCCGC
 6791 GTGGCGCTGC TGGAGATGGC GGACCGATG GATATGTTCT GCACAGGGTTT GGTTTGCAGA TTACAGTT
 6861 TCCGCAAGAA TTGATTGGCT CCAATTCTG GAGTGGTGA TCCGTTAGCG AGGCCATCCA GCCTCGCGTC
 6931 GAACTAGATG ATCCGCTGTG GAATGTGTG CAGTTAGGGT GTGAAAGTC CCCAGGCTCC CCAGCAGGCA
 7001 GAAAGTAGCA AACGATCATC CTCAATTAG CAGCAACCG GTGTTGAAAG TCCCAGGCT CCCCAGCAGG
 7071 CAGAAGTAGT CAAACATGC ATCTCAATTAG TGCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG
 7141 CCCCTAACTC CGCCCAAGTTC CGCCCAATTCT CCGCCCATG GCTGACTAAT TTTTTTATT TATGCAGAGG
 7211 CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTTGGAGGGT GACGCCACG
 7281 ACCGGTCCG CCACCATCCC CTGACCCACG CCCCTGACCC CTACAAGGA GACGACCTTC CATGACCGAG
 7351 TACAAGCCCA CGGTGCGCT CGCCACCCCG GACGACGTC CCGGGCGCTG ACAGCACCTC GCCGCCCGT
 7421 TCGCCGACTA CCGCCACCG CGCCACACCG TCGACCCCGA CCGCCACATC GAACCGTCA CCGAGCTGCA
 7491 AGAACTCTTC CTCACCGCG TCGGGCTCGA CATCGGCAAG GTGTTGGTCG CGGACGACGG CGCCGCGGTG
 7561 GCGCTCTGGA CACCGCCGGA GAGCGTCAAGA GCGGGGGCGG TGTGCGCGA GATCGCCCG CGCATGGCC
 7631 AGTTGAGCGG TTCCCGCTG GCGCGCGC AACAGATGGA AGGCGCTCTG GCGCCGCACC GGCCCAAGGA
 7701 GCGGGCTGG TTCTCTGGCA CCGTCGGCT CTCGCCCCGAC CACCAAGGGCA AGGGCTGG CAGGCCGTC
 7771 GTGCTCCCCG GAGTGGAGGC GGCGAGCGC GCGGGGTGC CCGCTTCTC GGAGACCTCC GCGCCCCGCA
 7841 ACCCTCCCTT CTACGACGG CTCGGCTTCA CCGTCACCGC CGACGTCGAG TGCCGAAGG ACCGCGCGAC
 7911 CTGGTCATG ACCCGCAAGC CCGGGTCTG ACGCCCGGG CACGACCCCG AGCGCCCGAC CGAAAGGAGC
 7981 GCACGACCCG GTCCGCGCG GGGCCACCGG TCCCAGGGGG TGCGACCTCG AAACCTGTTT ATTGCAGCTT
 8051 ATAATGGTTA CAAATAAGC AATAGCATCA CAAATTTCAC AAATAAGCA TTTTTTAC TGCATTCTAG
 8121 TTGTGGTTG TCCAAACTCA TCAATGTATC TTATCATGTC TGATCGATC CGAACCCCTT CCTCGACCAA
 8191 TTCTCATGTT TGACAGCTTA TCATCGAGA TCCGGGCAAC GTTGTGTCAT TGCTGAGGC GCAGAACTGG
 8261 TAGGTATGGA AGATCTATAC ATTGAATCAA TATTGGCAAT TAGCATGTT ATGTACATT ATATTGGCTC
 8331 AAATCAATAT TGGCTATTGG CCATTGACATA CGTTGTATCT ATATCATAAT ATGTACATT ATATTGGCTC
 8401 ATGTCCAATA TGACCGCCAT GTTGACATTG ATTATGACT AGTTATTAAAT AGTAATCAAT TACGGGGTCA
 8471 TTAGTCATCA GCCCCATATAG GGAGTCTCGC GTTACATACAG TTACGGTAAAG TGGCCCGCCT GGCTGACCGC
 8541 CCAAGACCC CGGCCATTG ACGTCAATAA TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA
 8611 TTGACGTCAA TGGGTGGAGT ATTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGT TAATATGCCA
 8681 AGTCGCCCC CTATTGACGT CAATGACGGT AAATGCCCG CCTGGCATTA TGCCCACTAC ATGACCTTAC
 8751 GGGACTTTCTC TACTTGGCAG TACATCTACG TATTAGTCAT CGCTATTACG ATGGTGTATGC GGTTTGGCA
 8821 GTACACCAAT GGGCGTGGAT AGCGGTTGTA CTCAGGGGGA TTTCAGGTC TCCACCCCAT TGACGTCAT
 8891 GGGAGTTGT TTGGCACCAGA AAATCACCG GACTTCCAA AATGTCGTAA TAACCCGCC CGTTGACGC
 8961 AAATGGCGG TAGGCGTGTG CGGTGGGAGG TCTATATAAG CAGAGCTCGT TTAGTGAACC GTCAAGATCTC
 9031 TAGAAGCTGG GTACCGGGAT CCAGCAGCTG GGCTCGAGGT GCTAGCGGGA GGGGGTGGAT GTGGGATCGA
 9101 AGGTGCGAAC CTTACTCACA CATGCCACCG TGACCCACG CCTGAAGCC AGGGGGCACC GTCACTCTTC
 9171 CTCTTCCCCC CAAAAACCCCA GGACACCCCT ATGATCTCCC GGACACCTGAA GTTCACATGC GTGGTGGTGG
 9241 ACGTGAGCCA CGAAGACCC GAGGTCAAGT TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA
 9311 GACAAGCCG CGGGAGGAGC AGTACAACAG CACGTCACCGT GTGGTCAAGC TCCTCACCGT CCTGCACCG
 9381 GACTGGTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCA ACAAAAGCCCT CCCAGCCTCC ATCGAGAAAAA
 9451 CCATCTCAA AGGCAAGAGG CAGCCCGAG AACACACGGT GTACACCCCT CCCCCCATCCC GGGATGAGCT
 9521 GACCAAGAAC CAGGTCAAGC TGACCTGCC GGTCAAAGGC TTCTATCCCA GCGACATCGC CGTGGAGTGG
 9591 GAGAGCAATG GGCAGCCGA GAACAACACT AACAGCACCGC CTCCCGTGTG GGACTCCGAC GGCTCCCTCT
 9661 TCCTCTACAG CAAGCTCACCG GTGGACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT GCTCCGTGAT
 9731 GCATGAGGCT CTGCACAAAC ACTACACCGA GAAGAGCCTC TCCCTGTCTC CGGGTAAATG ACTCGAGGCC
 9801 CGAACAAAAA CTCATCTCAAG AAGAGGATCT GAATAGCGCC GTCGACCATC ATCATCATCA TCATTGAGTT
 9871 TNAACGATCC AGACATGATA AGATACATTG ATGAGTTGG ACAAAACCACAA ACTAGAATGC AGTGAAGAAA
 9941 ATGCTTTATT TGTGAAATTG TGATGCTAT TGCTTATTAA GTAACCCATTA TAAGCTGCAA TAAACAAGTT
 10011 AACAAACAACAA ATTGCAATTCA TTTTATGTTT CAGCTTCAAG GGGAGGTGGG GAGGTTTTT AAAGCAAGTA
 10081 AACACCTCTAC AAATGTGGTA TGGCTGATTA TGATCCGGCT GCCTCGGGCG TTTCGGTGAT GACGGTGGAAA
 10151 ACCTCTGACA CATGCAGCTC CGGGAGACGG TCACAGCTTG TCTGTAAGCG GATGCCGGGA GCAGACAAGC
 10221 CGTCAGGGC CGCTCAGCGG GTGTTGGCGG GTGTCGGGGC GCAGCCATGA CGGGTCGACT CTAGA

284:

5'LT• : (SEQ ID NO:284)

5'-CTT GGT GCC GCA GGA TCA G-3'

285:

3'LT• : (SEQ ID NO:285)

5'-CAG ATG GCT GTC ACC CCA C-3'

286:

5'LT• long-*NheI*: (SEQ ID NO:286)

5'-GCC CGC TAG CCT GCG GTG GTC AGG ATC AGG GAC GTC G-3'

287:

5'LT• short-*NheI*: (SEQ ID NO:287)

5'-GCC CGC TAG CCT GCG GTG GTT CTC CAG CTG CGG ATT C -3'

288:

3'LT• stop-*NotI*: (SEQ ID NO:288)

5'-CAA TGA CTG CGG CCG CTT ACC CCA CCA TCA CCG -3'

289:

GST-EK-C-LT• ₄₉₋₃₀₆: SEQ ID NO:289

APLVMSPLGYWKIGLVPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRGVSRRIAYSKDFETLKVDFLSKLPEMLKMFDRLCH
KTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQAKRQLDDSKPSCILPSPSSL
SETPDPRLHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDGVQQLPKGEPETDLNPEL
PAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPPAGRSPRARS
LTLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGY GSLWYTSVGFGLAQLRSGERVYVNISHPDMV
DYRRGKTFFGAVMVG

290:

GST-EK-C-LT• ₁₂₆₋₃₀₆: SEQ ID NO:290

APLVMSPILGWIKGLVQPTRLLEYLEEKYEEHYERDEGDKWRNKKFELGLEFPNLPPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIYGVSRAYSQDFETLKVDFLSKLPEMLKMFEDRLCH
KTYLNGDHVTPDFMLYDALDVLYMDPMCLDAFPKLVCFKKRIEAPIQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGVQQLPKGEPETDLNPELPAAHLIGA
WMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPPAGRSRARSLLRSALY
RAGGAYGRGSPELLLEGAETVTPVVDPIGY GSLWYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKT
FFGAVMVG

291:

his-myc-EK-C-LT• 49-306: SEQ ID NO:291

APLVHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQ
AQKRLDDSKPSCILPSPLLSETPDPRHLQRSNASRNLASTSQGPVAQSSREASAWMTSPAADSTPDGV
QQLPKGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGY
RGRTPPAGRSRARSLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGY GSLWYTSVGFGLAQLRSGERVY
VNISHPDMVDYRRGKTFFGAVMVG

292:

his-myc-EK-C-LT• 126-306: SEQ ID NO:292

APLVHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGVQQLP
KGEPETDLNPELPAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRT
PPAGRSRARSLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIGY GSLWYTSVGFGLAQLRSGERVY
VNISHPDMVDYRRGKTFFGAVMVG

293:

primerMCS-1F

5'-TAT GGA TCC GGC TAG CGC TCG AGG GTT TAA ACG GCG GCC GCA T-3' (SEQ ID NO:293)

294:

primerMCS-1R

5'-TCG AAT GCG GCC GCC GTT TAA ACC CTC GAG CGC TAG CCG GAT CCA-3' (SEQ ID NO:294)

295:

Bamhis6-EK-Nhe-F

5'-GAT CCA CAC CAC CAC CAC CAC GGT TCT GGT GAC GAC GAT GAC AAA GCG CTA GCC C-3'
(SEQ ID NO:295)

296:

Bamhis6-EK-Nhe-R

5'-TCG AGG GCT AGC GCT TTG TCA TCG TCG TCA CCA GAA CCG TGG TGG TGG TGG TGG TGT G-3'
(SEQ ID NO:296)

297:

oligo1F-C-glycine-linker

5'-TCG AGG GTG GTG GTG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:297)

BAMHIS6-EK-NHE-R

298:

oligo1R-C-glycine-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCA CCA CCC-3' (SEQ ID NO:298)

299:

oligo1F-C-gamma1-linker

5'-TCG AGG ATA AAA CCC ACA CCT CTC CGC CGT GTG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:299)

300:

oligo1R-C-gamma1-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCA CAC GGC GGA GAG GTG TGG GTT TTA TCC-3' (SEQ ID NO:300)

301:

oligo1FA-C-gamma3-linker

5'-TCG AGC CGA AAC CGT CTA CCC CGC CGG GTT CTT CTG-3' (SEQ ID NO:301)

302:

oligo1RA-C-gamma3-linker

5'-CAC CAC CAG AAG AAC CCG GCG GGG TAG ACG GTT TCG GC-3' (SEQ ID NO:302)

303:

oligo2FB-C-gamma3-linker

5'-GTG GTG CTC CGG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:303)

304:

oligo2RB-C-gamma3-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCC GGA G-3' (SEQ ID NO:304)

305:

rMIF-F

5'-GGA ATT CCA TAT GCC TAT GTT CAT CGT GAA CAC-3' (SEQ ID NO:305)

306:

rMIF-Xho-R

5'-CCC GCT CGA GAG CGA AGG TGG AAC CGT TC-3' (SEQ ID NO:306)

307:

rMIF-C1:

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYDMNAANVGWNGSTFALEGGGGGCG (SEQ ID NO:307)

308:

rMIF-C2

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYDMNAANVGWNGSTFALEDKTHTSPPCG (SEQ ID NO:308)

309:

rMIF-C3

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDRVYINYDMNAANVGWNGSTFALEPKPSTPPGSSGGAPGGCG (SEQ ID
NO:309)

310:

met-human-MIF-C1

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEGGGGGCG

311:

human-MIF-C1 (SEQ ID NO:311)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEGGGGGCG

312:

met-human-MIF-C2 (SEQ ID NO:312)

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEDKTHTSPPCG

313:

human-MIF-C2 (SEQ ID NO:313)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEDKTHTSPPCG

314:

met-human-MIF-C3 (SEQ ID NO:314)

MPMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRISPDRVYINYYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG

315:

human-MIF-C3 (SEQ ID NO:315)

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRYSKLLC GLLAERLRISPDRVYINYYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG

316:

RANKL-UP:

5'CTGCCAGGGCCGGTGCGCGGGCATCATCACCAACCACCAAGCGTTCTCAGGAG-3'

317:

RANKL-DOWN :

5'-CCGCTCGAGTTAGTCTATGTCCTGAACCTTGAAAG-3'

318 and 319:

Protein sequence of GST-PS-C-RANKL (SEQ ID NO:318; capital letters)

cDNA sequence of GST-PS-C-RANKL (SEQ ID NO:319; small letters)

M S P I L G Y W K I K G L V Q P T R L L L E Y L E
1 atgtcccccataacttaggttattggaaaattaaggccctgtcaacccactcgacttctttggaaatatctgaa
26 E K Y E E H L Y E R D E G D K W R N K K F E L G L
76 gaaaaatataaagagcatttgttatgagcgcgatgaaggtataatggcggaaacaaaagttgaattgggttg
51 E F P N L P Y Y I D G D V K L T Q S M A I I R Y I
151 gagtttcccaatcttcattatattatgtatggatgtttaaaatcacatgtcatggccatcatacgttatata
76 A D K H N M L G G C P K E R A E I S M ' L E G A V L
226 gctgacaaggacaacatgttgggtgggtccaaaagagcgtgcagagatttcaatgttgaaggagcggtttg
101 D I R Y G V S R I A Y S K D F E T L K V D F L S K
301 gatattagataggcgtttcgagattgtatagtaaagactttggaaacttcaaagtgtttagcaag
126 L P E M L K M F E D R L C H K T Y L N G D H V T H
376 ctacctgaaatgtcgtaaaatgttcaagatcgttatgtcataaaacatatttaaatggatcatgtaccat
151 P D F M L Y D A L D V V Y M D P M C L D A F P K
451 cctgacttcatgttgcacgtgttgcacgtgttgcacgtgttgcacgtgttgcacgtgttgcacgtgttgcacgt
176 L V C F K K R I E A I P Q I D K Y L K S S K Y I A
526 ttagttgtttaaaaaacgtattgaagctatcccacaaattgataagtaacttgcacgttatata
201 W P L Q G W Q A T F G G G D H P P K S D L E V L F
601 tggcccttgcaggcgtggcaaggccacgttgggtggcggccatctccaaaatcgatctggaaatccacgttat
226 Q G P G C G G G H H H H Q R F S G A P A M M E
676 caGGGGCCCGGGTGCAGCGGTGGCATCATCACCACCATCACCAAGCGCTCTCAGGAGCTCCAGCTATGAA
251 G S W L D V A Q R G K P E A Q P F A H L T I N A A
751 GGCTCATGGTGGATGTGGCCAGCGAGGCAAGGCCAGCTGGCCACACCTCACCATCAATGCTGCC
276 S I P S G S R K V T L S W Y H D R G W A K I S N
826 AGCATCCCATCGGGTCCCCATAAAGTCACTCTGCTCTTGGTACACGATCGAGGCTGGCCAAGATCTAAC
301 M T L S N G K L R V N Q D G F Y Y L Y A N I C F R
901 ATGACGTTAACGAAACGAAACTAACGGTTAACCAAGATGGCTTATTACCTGTACGCCAACATTGCTTCGG
326 H H E T S G S V P T D Y L Q L M V Y V V K T S I K
976 CATCATGAAACATCGGGAAAGCGTACCTACAGACTATCTCAGCTGTGGTATGCGTAAACCCAGCATCAA
351 I P S S H N L M K G G S T K N W S G N S E F H F Y
1051 ATCCCAAGTTCTCATAACCTGATGAAAGGGAGGAGCACGAAAAACTGGTGGCAATTCTGAATTCCACTTTAT
376 S I N V G G F K R A G E E I S T Q V S N P S L
1126 TCCATAAATGTTGGGGGATTTCAAGCTCCAGCTGGTAAGAAATTAGCATCAGGTGTCACCCCTCCCTG
401 L D P D Q D A T Y F G A F K V Q D I D *
1201 CTGGATCCGGATCAAGATGCGACGTACTTGGGCTTCAAAGTTCAAGGACATAGACTAACTCGAGCGG

320:

Human-C-RANKL

GCAGGGQHRAEKAMVDGSWLDLAKRSKLEAQPFKAHLTINATDIPSGSHKVSLSSWYHDRGWAKISNMTFSNGKLI
VNQDGFYLYANICFRHHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHYSINVGGFFK
LRSGEEISIEVSNPSLLDPDQDATYFGAFKVRDID

321:

Primer 5'PrP-BamHI

5'-CGG GAT CCC ACC ATG GTG GGG GGC CTT GG -3' (SEQ ID NO:321)

322:

Primer 3'PrP-NheI

5'-CTA GCT AGC CTG GAT CTT CTC CCG -3' (SEQ ID NO:322)

323:

Protein sequence of mPrP_t-EK-Fc*

MVGGLGGYMLGSAMSRPMIHFGNWDERYYRENMYRYPNQVYRVDQYSNQNNFVHDCVNITIKQHT
VTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYDGRSRLAGGGCGDDDKLTHTCPCPAPEA
EGAPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
K

324:

mPrP_t

MVGGLGGYMLGSAMSRPMIHFGNWDERYYRENMYRYPNQVYRVDQYSNQNNFVHDCVNITIKQHT
VTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYDGRSRLAGGGCGDDDK

325:

human resistin-C-Xa: (SEQ ID NO:325)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQS VTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
IEGR

326:

human resistin-C-EK: (SEQ ID NO:326)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQS VTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
DDDK

327:

human resistin-C: (SEQ ID NO:327)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQS VTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG

328:

mouse C-IL-13-F: (SEQ ID NO:328)

ADPGGGGGLAGPVRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSLTNISNCN
AIYRTQRILHGLCNRKAPTTVSSLPTDKIEVAHFITKLLSYTKQLFRHGPFLEVLAIEGR
329:

mouse C-IL-13-S: (SEQ ID NO:329)

LACGGGGGPVRSVSLPLTLKELIEELSNITQDQTPLCNGSMVWSVDLAAGGFCVALDSLTNISNCNAI
YRTQRILHGLCNRKAPTTVSSLPTDKIEVAHFITKLLSYTKQLFRHGPF

330:

human C-IL-13-F: (SEQ ID NO:330)

ADPGGGGGLAGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCS
AIEKTQRMLSGFCPHKVSAQGFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRFNLEVLAIEGR

331:

human C-IL-13-S: (SEQ ID NO:331)

LACGGGGGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQR
MLSGFCPHKVSAQGFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRFN

332:

mouse C-IL-5-E: (SEQ ID NO:332)

ALVGCGGPKPSTPPGSSGGAPASMEIPMSTVVKETLTQLSAHALLTSNETMRLPVPTHKNHQLCIGEIFQG
LDILKNQTVRGGTVEMLFQNLNSLIKYYIDRQKEKCIGEERRTRQFLDYLQEFLGVMSTEWAMEG

333:

mouse C-IL-5-F: (SEQ ID NO:333)

ADPGGGGGLAMEIPMSTVVKETLTQLSAHALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVR
GGTVEMLFQNLNSLIKYYIDRQKEKCIGEERRTRQFLDYLQEFLGVMSTEWAMEGLEVLIAEGR

334:

mouse C-IL-5-S: (SEQ ID NO:334)

LACGGGGGMEIPMSTVVKETLTQLSAHALLTSNETMRLPVPTHKNHQLCIGEIFQGLDILKNQTVRG
TVEMLFQNLNSLIKYYIDRQKEKCIGEERRTRQFLDYLQEFLGVMSTEWAMEG

335:

human C-IL-5-E: (SEQ ID NO:335)

ALVGCGGPKPSTPPGSSGGAPASIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPHKNHQLCTEEIFQGI
GTLESQTVQGGTVERLFKNLNSLIKYYIDGQKKCGEERRRNQFLDYLQEFLGVMNTIEW IES

336:

human C-IL-5-F: (SEQ ID NO:336)

ADPGCGGGGLAIPTEIPSTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGG
GTVERLFKNLSLIKYYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES LEVLAIEGR

337:

human C-IL-5-S: (SEQ ID NO:337)

LACGGGGIPTEIPSTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGT
VERLFKNLSLIKYYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES

338:

primer NheIL13-F: (SEQ ID NO:338)

CTAGCTAGCCGGGCCGGTGCCAAGATC

339:

primer XhoIL13-R: (SEQ ID NO:339)

TTTCTCGAGGAAGGGGCCGTGGCGAA

340:

primer Spelinker3-F1: (SEQ ID NO:340)

CCCCGCCGGTTCTCTGGCGGTGCTCCGGTAGCATGGAGATTCCATGAGCAC

341:

Primer SpeNlinker3-F2: (SEQ ID NO:341)

TTTTACTAGTTGGTTGC GGCGGCCGAAACCGAGCACCCCGCCGGTTCTTC

342:

Primer IL5StopXho-R: (SEQ ID NO:342)

TTTGCGGCCGCGTTAAACTCGAGTTATTAGCCTTCCATTGCCCACTC

343:

Primer BamH1-FLK1-F: (SEQ ID NO:343)

CGCGGATCCATTCATGCCCTCTGTC

344:

Primer Nhe1-FLK1-B: (SEQ ID NO:344)

CTAGCTAGCTTGTGTGAACCTGGAC

345:

mVEGFR-2 (2-3) fragment: (SEQ ID NO:345)

PFIAS VSDQHGIVYI TENKNKTVVI PCRGSISNLN VSLCARYPEK RFVPDGNRIS WDSEIGFTLP
SYMISYAGMV FCEAKINDET YQSIMYIVVV VGYRIYDVIL SPPHEIELSA GEKLVLNCTA
RTELNVGLDF TWHSSPSKSH HKKIVNRDVK PFPGTVAKMF LSTLTIESVT KSDQGEYTCV
ASSGRMIKRN RTFVRVHTKP

346

human C-LT[•] 49-306 : (SEQ ID NO:346)

LACGGQDQGRRVEKIIQSGAQAKRLDDSKPSCILPSPSSLSETPDPRLHPQRSNASRNLASTSQGPVAQSSR
EASAWMTILSPAADSTPDGVQQLPKGEPETDLNPELPAAHЛИAWMSGQGLSWEASQEEFLRSGAQFSP
THGLALPQDGVYYLYCHVGYRGRTPPAGRSRARSLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIG
YGSLWYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

347

human C-LT[•] 126-306 : (SEQ ID NO:347)

LACGGSPAADSTPDGVQQLPKGEPETDLNPELPAAHЛИAWMSGQGLSWEASQEEFLRSGAQFSP
THGLALPQDGVYYLYCHVGYRGRTPPAGRSRARSLLRSALYRAGGAYGRGSPELLLEGAETVTPVVDPIG
YGSLWYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

348

Modified human prion protein fragment: (SEQ ID NO:348)

VGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMRYPNQVYYRPMD
YSNQNNFVHDCVNITIKQHTVTTTKGENFTETDVKMMERVVEQMCITQYERESQAYYQ
RGRLAGGGCG

349

Modified bovine prion protein fragment: (SEQ ID NO:349)

VGGLGGYMLGSAMSRPLIHFGSDYEDRYYRENMRYPNQVYYRPVDQ
YSNQNNFVHDCVNITVKQHTVTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQ
RGRLAGGGCG

350

Modified sheep prion protein fragment: (SEQ ID NO:350)

VGGLGGYMLGSAMSRPLIHFGNDYEDRYYRENMYRYPNQVYYRPVDR
YSNQNNFVHDCVNITVKQHTVTTTKGENFTETDIKIMERVVEQMCITQYQRESQAYYQ
RGRLAGGGCG